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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS

(57) Abstract: The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, transformed eukaryotic cells expressing these DNAs and antibodies directed to these proteins.

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DESCRIPTION

Human Proteins Having Hydrophobic

Domains and DNAs Encoding These Proteins

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TECHNICAL FIELD

The present invention relates to human proteins

having hydrophobic domains, DNAs encoding these proteins,

expression vectors for these DNAs, eukaryotic cells

10   expressing these DNAs and antibodies directed to these

proteins. The proteins of the present invention can be

employed as pharmaceuticals or as antigens for preparing

antibodies directed to these proteins. The human cDNAs of

the present invention can be utilized as probes for genetic

15   diagnosis and gene sources for gene therapy. Furthermore,

the cDNAs can be utilized as gene sources for producing the

proteins encoded by these cDNAs in large quantities. Cells

into which these genes are introduced to express secretory

proteins or membrane proteins in large quantities can be

20   utilized for detection of the corresponding receptors or

ligands, screening of novel small molecule pharmaceuticals

and the like. The antibodies of the present invention can be

utilized for the detection, quantification, purification and

the like of the proteins of the present invention.

25

BACKGROUND ART

Cells secrete many proteins extracellularly. These secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport, the biophylaxis, and the like of the cells. Unlike intracellular proteins, the secretory proteins exert their actions outside the cells. Therefore, they can be administered in the intracorporeal manner such as the injection or the drip, so that they possess hidden potentialities as pharmaceuticals. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents and the like are currently employed as pharmaceuticals. In addition, secretory proteins other than those described above are undergoing clinical trials for developing their use as pharmaceuticals. It is believed that the human cells produce many unknown secretory proteins. Availability of these secretory proteins as well as genes encoding them is expected to lead to development of novel pharmaceuticals utilizing them.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters and the like in the material transport and the signal transduction through the cell membrane. Examples thereof include receptors for various cytokines, ion

channels for the sodium ion, the potassium ion, the chloride

ion and the like, transporters for saccharides and amino

acids and the like. The genes for many of them have already

been cloned. It has been clarified that abnormalities in

these membrane proteins are involved in a number of

previously cryptogenic diseases. Therefore, discovery of a

new membrane protein is expected to lead to elucidation of

the causes of many diseases, so that isolation of new genes

encoding the membrane proteins has been desired.

Heretofore, due to difficulty in the purification

from human cells, many of these secretory proteins and

membrane proteins have been isolated by genetic approaches.

A general method is the so-called expression cloning method,

in which a cDNA library is introduced into eukaryotic cells

to express cDNAs, and the cells secreting, or expressing on

the surface of membrane, the protein having the activity of

interest are then screened. However, only genes for proteins

with known functions can be cloned by using this method.

In general, a secretory protein or a membrane

protein possesses at least one hydrophobic domain within the

protein. After synthesis on ribosomes, such domain works as

a secretory signal or remains in the phospholipid membrane

to be entrapped in the membrane. Accordingly, if the

existence of a highly hydrophobic domain is observed in the

amino acid sequence of a protein encoded by a cDNA when the

whole base sequence of the full-length cDNA is determined,
it is considered that the cDNA encodes a secretory protein
or a membrane protein.

5   OBJECTS OF INVENTION

        The main object of the present invention is to
provide novel human proteins having hydrophobic domains,
DNAs encoding these proteins, expression vectors for these
DNAs, transformed eukaryotic cells that are capable of
10   expressing these DNAs and antibodies directed to these
proteins. This object as well as other objects and
advantages of the present invention will become apparent to
those skilled in the art from the following description with
reference to the accompanying drawings.

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     SUMMARY OF INVENTION

        As the result of intensive studies, the present
inventors have successfully cloned cDNAs encoding proteins
having hydrophobic domains from the human full-length cDNA
20   bank, thereby completing the present invention. Thus, the
present invention provides a human protein having
hydrophobic domain(s), namely a protein comprising any one
of an amino acid sequence selected from the group consisting
of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and
25   121 to 130. Moreover, the present invention provides a DNA

encoding said protein, exemplified by a cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150, an expression vector that is capable of expressing

5   said DNA by in vitro translation or in eukaryotic cells, a transformed eukaryotic cell that is capable of expressing said DNA and of producing said protein and an antibody directed to said protein.

10   BRIEF DESCRIPTION OF DRAWINGS

Fig.   1   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03171.

Fig.   2   illustrates   the

15   hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03424.

Fig.   3   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03444.

20   Fig.   4   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03478.

Fig.   5   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded

25   by clone HP03499.

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Fig. 6 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03500.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10691.

Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10703.

Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10711.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10712.

Fig. 11 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03010.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03576.

Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03611.

Fig. 14 illustrates the

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hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03612.

Fig.   15   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10407.

Fig.   16   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10713.

Fig.   17   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10714.

Fig.   18   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10716.

Fig.   19   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10717.

Fig.   20   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10718.

Fig.   21   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03745.

Fig.   22   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded

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by clone HP03747.

Fig.   23   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10719.

5   Fig.   24   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10720.

Fig.   25   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded 10   by clone HP10721.

Fig.   26   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10725.

Fig.   27   illustrates   the 15   hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10727.

Fig.   28   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10728.

20   Fig.   29   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10730.

Fig.   30   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded 25   by clone HP10742.

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        Fig.   31   illustrates   the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03800.

        Fig.   32   illustrates   the
5   hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03831.

        Fig.   33   illustrates   the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03879.

10   Fig.   34   illustrates   the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03880.

        Fig.   35   illustrates   the
hydrophobicity/hydrophilicity profile of the protein encoded
15   by clone HP10704.

        Fig.   36   illustrates   the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10715.

        Fig.   37   illustrates   the
20   hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10724.

        Fig.   38   illustrates   the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10733.

25   Fig.   39   illustrates   the

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hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10734.

Fig. 40 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10756.

Fig. 41 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03670.

Fig. 42 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03688.

Fig. 43 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03825

Fig. 44 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03877.

Fig. 45 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10765.

Fig. 46 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10766.

Fig. 47 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded

by clone HP10770.

Fig.   48   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10772.

5   Fig.   49   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10773.

Fig.   50   illustrates   the hydrophobicity/hydrophilicity profile of the protein encoded

10   by clone HP10776.

DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolating proteins

15   from human organs, cell lines or the like, a method for preparing peptides by the chemical synthesis based on the amino acid sequences of the present invention, or a method for producing proteins by the recombinant DNA technology using the DNAs encoding the hydrophobic domains of the

20   present invention. Among these, the method for producing proteins by the recombinant DNA technology is preferably employed. For example, the proteins can be expressed in vitro by preparing an RNA by in vitro transcription from a vector having the cDNA of the present invention, and then

25   carrying out in vitro translation using this RNA as a

template. Alternatively, incorporation of the translated region into a suitable expression vector by the method known in the art may lead to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia*

5   *coli, Bacillus subtilis*, etc., and eukaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where the protein of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be

10 produced in vitro by incorporating the translated region of this cDNA into a vector having an RNA polymerase promoter, and then adding the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, which contains an RNA polymerase corresponding to the

15 promoter. The RNA polymerase promoters are exemplified by T7, T3, SP6 and the like. The vectors containing promoters for these RNA polymerases are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II and the like. Furthermore, the protein of the present invention can be expressed in the

20 secreted form or the form incorporated in the microsome membrane when a canine pancreas microsome or the like is added to the reaction system.

In the case where the protein of the present invention is produced by expressing the DNA in a

25 microorganism such as *Escherichia coli* etc., a recombinant

expression vector in which the translated region of the cDNA of the present invention is incorporated into an expression vector having an origin which is capable of replicating in the microorganism, a promoter, a ribosome-binding site, a

5   cDNA-cloning site, a terminator and the like is constructed. After transformation of the host cells with this expression vector, the resulting transformant is cultivated, whereby the protein encoded by the cDNA can be produced in large quantities in the microorganism. In this case, a protein

10   fragment containing any translated region can be obtained by adding an initiation codon and a termination codon in front of and behind the selected translated region to express the protein. Alternatively, the protein can be expressed as a fusion protein with another protein. Only the portion of the

15   protein encoded by the cDNA can be obtained by cleaving this fusion protein with a suitable protease. The expression vectors for *Escherichia coli* are exemplified by the pUC series, pBluescript II, the pET expression system, the pGEX expression system and the like.

20   In the case where the protein of the present invention is produced by expressing the DNA in eukaryotic cells, the protein of the present invention can be produced as a secretory protein, or as a membrane protein on the surface of cell membrane, by incorporating the translated

25   region of the cDNA into an expression vector for eukaryotic

cells that has a promoter, a splicing region, a poly(A) addition site and the like, and then introducing the vector into the eukaryotic cells. The expression vectors are exemplified by pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL,

5 pBK-CMV, pBK-RSV, EBV vectors, pRS, pYES2 and the like. Examples of eukaryotic cells to be used in general include mammalian cultured cells such as monkey kidney COS7 cells, Chinese hamster ovary CHO cells and the like, budding yeasts, fission yeasts, silkworm cells, Xenopus oocytes and the like.

10 Any eukaryotic cells may be used as long as they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eukaryotic cells by using a method known in the art such as the electroporation method, the calcium phosphate method, the

15 liposome method, the DEAE-dextran method and the like.

After the protein of the present invention is expressed in prokaryotic cells or eukaryotic cells, the protein of interest can be isolated and purified from the culture by a combination of separation procedures known in

20 the art. Examples of the separation procedures include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric

25 focusing, ion-exchange chromatography, hydrophobic

chromatography, affinity chromatography, reverse phase chromatography and the like.

The proteins of the present invention also include peptide fragments (of 5 amino acid residues or more) containing any partial amino acid sequences in the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the protein of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP-A 8-187100]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secreted forms. Such proteins or peptides in the secreted forms shall also come within the scope of the protein of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences of the proteins, expression of the proteins in appropriate eukaryotic cells affords the proteins to which sugar chains are added. Accordingly, such proteins or peptides to which sugar chains are added shall also come

within the scope of the protein of the present invention.

The DNAs of the present invention include all the DNAs encoding the above-mentioned proteins. These DNAs can be obtained by using a method for chemical synthesis, a method for cDNA cloning and the like.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. The cDNAs are synthesized by using poly(A)$^+$ RNAs extracted from human cells as templates. The human cells may be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method such as the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and Hoffman, J., Gene 25: 263-269 (1983)] and the like. However, it is desirable to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available human cDNA libraries can be utilized. The cDNAs of the present invention can be cloned from the cDNA libraries by synthesizing an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention and screening the cDNA libraries using this oligonucleotide as a probe for colony or plaque hybridization according to a method known

in the art. In addition, the cDNA fragments of the present

invention can be prepared from an mRNA isolated from human

cells by the RT-PCR method in which oligonucleotides which

hybridize with both termini of the cDNA fragment of interest

5   are synthesized, which oligonucleotides are then used as the

primers.

The   cDNAs   of   the   present   invention   are

characterized in that they comprise any one of the base

sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71

10   to 80, 101 to 110 and 131 to 140 or the base sequences

represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111

to 120 and 141 to 150. Tables 1 and 2 summarizes the clone

number (HP number), the cell from which the cDNA clone was

obtained, the total number of bases of the cDNA, and the

15   number of the amino acid residues of the encoded protein,

for each of the cDNAs.

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Table 1

SEQ ID NO.			HP number	Cell	Number of bases	Number of amino acid residues
1,	11,	21	HP03171	Thymus	2042	267
2,	12,	22	HP03424	Liver	1433	419
3,	13,	23	HP03444	Kidney	1917	415
4,	14,	24	HP03478	Umbilical cord blood	2258	380
5,	15,	25	HP03499	Kidney	1973	585
6,	16,	26	HP03500	kidney	1606	331
7,	17,	27	HP10691	Umbilical cord blood	2380	345
8,	18,	28	HP10703	Kidney	2017	89
9,	19,	29	HP10711	Kidney	1606	406
10,	20,	30	HP10712	Kidney	1695	192
31,	41,	51	HP03010	Kidney	1551	377
32,	42,	52	HP03576	Kidney	1713	81
33,	43,	53	HP03611	Kidney	1758	487
34,	44,	54	HP03612	Kidney	1550	375
35,	45,	55	HP10407	Stomach cancer	1485	350
36,	46,	56	HP10713	Kidney	2694	667
37,	47,	57	HP10714	Umbilical cord blood	3297	464
38,	48,	58	HP10716	Umbilical cord blood	2126	470
39,	49,	59	HP10717	Kidney	1781	243
40,	50,	60	HP10718	Umbilical cord blood	1788	270
61,	71,	81	HP03745	Kidney	1376	389
62,	72,	82	HP03747	Umbilical cord blood	2392	348
63,	73,	83	HP10719	Kidney	1416	261
64,	74,	84	HP10720	Kidney	1347	222
65,	75,	85	HP10721	Kidney	2284	183

Table 2

SEQ ID NO	HP number	Cell	Number of bases	Number of amino acid residues
66, 76, 86	HP10725	Kidney	1737	262
67, 77, 87	HP10727	Umbilical cord blood	1556	168
68, 78, 88	HP10728	Umbilical cord blood	1855	243
69, 79, 89	HP10730	Umbilical cord blood	2530	428
70, 80, 90	HP10742	Umbilical cord blood	1911	283
91, 101, 111	HP03800	Umbilical cord blood	1633	476
92, 102, 112	HP03831	Kidney	1095	226
93, 103, 113	HP03879	Kidney	1602	305
94, 104, 114	HP03880	Kidney	897	227
95, 105, 115	HP10704	Kidney	1866	441
96, 106, 116	HP10715	Umbilical cord blood	2198	265
97, 107, 117	HP10724	Umbilical cord blood	2180	208
98, 108, 118	HP10733	Umbilical cord blood	1527	400
99, 109, 119	HP10734	Umbilical cord blood	1905	192
100, 110, 120	HP10756	Kidney	998	260
121, 131, 141	HP03670	Umbilical cord blood	1622	337
122, 132, 142	HP03688	Umbilical cord blood	2475	236
123, 133, 143	HP03825	Kidney	1739	560
124, 134, 144	HP03877	Kidney	2005	406
125, 135, 145	HP10765	Umbilical cord blood	1558	453
126, 136, 146	HP10766	Kidney	1005	59
127, 137, 147	HP10770	Kidney	969	210
128, 138, 148	HP10772	Kidney	1241	165
129, 139, 149	HP10773	Kidney	1174	162
130, 140, 150	HP10776	Kidney	1012	221

The same clones as the cDNAs of the present invention can be easily obtained by screening the cDNA libraries constructed from the human cell lines or human

tissues utilized in the present invention using an oligonucleotide probe synthesized on the basis of the base sequence of the cDNA provided in any one of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150.

5　　　　　In general, the polymorphism due to the individual differences is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are added, deleted and/or substituted with other nucleotides in SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131

10　　to 150 shall come within the scope of the present invention.

　　　　　　Similarly, any protein in which one or plural amino acids are added, deleted and/or substituted with other amino acids resulting from the above-mentioned changes shall come within the scope of the present invention, as long as

15　　the protein possesses the activity of the protein having any one of the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

　　　　　　The cDNAs of the present invention also include cDNA fragments (of 10 bp or more) containing any partial

20　　base sequence in the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140 or in the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Also, DNA fragments consisting of a sense strand and an anti-sense

25　　strand shall come within this scope. These DNA fragments can

be utilized as the probes for the genetic diagnosis.

The antibody of the present invention can be obtained from a serum after immunizing an animal using the protein of the present invention as an antigen. A peptide that is chemically synthesized based on the amino acid sequence of the present invention and a protein expressed in eukaryotic or prokaryotic cells can be used as an antigen. Alternatively, an antibody can be prepared by introducing the above-mentioned expression vector for eukaryotic cells into the muscle or the skin of an animal by injection or by using a gene gun and then collecting a serum therefrom (JP-A 7-313187). Animals that can be used include a mouse, a rat, a rabbit, a goat, a chicken and the like. A monoclonal antibody directed to the protein of the present invention can be produced by fusing B cells collected from the spleen of the immunized animal with myelomas to generate hybridomas.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for

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introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein

(such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation

Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol.

145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology
133:327-341, 1991; Bertagnolli, et al., J. Immunol.
149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-
1761, 1994.

5   Assays for cytokine production and/or
proliferation of spleen cells, lymph node cells or
thymocytes include, without limitation, those described in:
Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach,
E.M. In Current Protocols in Immunology. J.E.e.a. Coligan

10   eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto.
1994; and Measurement of mouse and human Interferon γ,
Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a.
Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons,
Toronto. 1994.

15   Assays for proliferation and differentiation of
hematopoietic and lymphopoietic cells include, without
limitation, those described in: Measurement of Human and
Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis,
L.S. and Lipsky, P.E. In Current Protocols in Immunology.

20   J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and
Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-
1211, 1991; Moreau et al., Nature 336:690-692, 1988;
Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-
2938, 1983; Measurement of mouse and human interleukin 6-

25   Nordan, R. In Current Protocols in Immunology. J.E.e.a.

Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In

5   Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark,S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John

10   Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include,

15   without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines

20   and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

25   <u>Immune Stimulating or Suppressing Activity</u>

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the

5   treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These

10   immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the

15   present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the

20   immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic

25   lupus erythematosus, rheumatoid arthritis, autoimmune

pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by

the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant.

Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of

5   repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in

10   preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have

15   been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven

20   Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases.

25   Many autoimmune disorders are the result of inappropriate

activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce

5   or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be

10   involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be

15   determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice

20   and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

       Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating

25   immune responses, may also be useful in therapy.

Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function

5   may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be

10   enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing

15   the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a

20   portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or

25   enhancement of antigen function (preferably B lymphocyte

antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a

cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;

Chapter 7, Immunologic studies in Humans); Herrmann et al.,
Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et
al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.
Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol.

5   137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512,
1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-
2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974,
1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai
et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J.

10   Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512,
1988; Bertagnolli et al., Cellular Immunology 133:327-341,
1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

         Assays   for   T-cell-dependent   immunoglobulin
responses and isotype switching (which will identify, among

15   others, proteins that modulate T-cell dependent antibody
responses and that affect Th1/Th2 profiles) include, without
limitation, those described in: Maliszewski, J. Immunol.
144:3028-3033, 1990; and Assays for B cell function: In
vitro antibody production, Mond, J.J. and Brunswick, M. In

20   Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1
pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

         Mixed lymphocyte reaction (MLR) assays (which will
identify, among others, proteins that generate predominantly
Th1 and CTL responses) include, without limitation, those

25   described in: Current Protocols in Immunology, Ed by J. E.

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Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W
Strober, Pub. Greene Publishing Associates and Wiley-
Interscience (Chapter 3, In Vitro assays for Mouse
Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies
in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986;
Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et
al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will
identify, among others, proteins expressed by dendritic
cells that activate naive T-cells) include, without
limitation, those described in: Guery et al., J. Immunol.
134:536-544, 1995; Inaba et al., Journal of Experimental
Medicine 173:549-559, 1991; Macatonia et al., Journal of
Immunology 154:5071-5079, 1995; Porgador et al., Journal of
Experimental Medicine 182:255-260, 1995; Nair et al.,
Journal of Virology 67:4062-4069, 1993; Huang et al.,
Science 264:961-965, 1994; Macatonia et al., Journal of
Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al.,
Journal of Clinical Investigation 94:797-807, 1994; and
Inaba et al., Journal of Experimental Medicine 172:631-640,
1990.

Assays for lymphocyte survival/apoptosis (which
will identify, among others, proteins that prevent apoptosis
after superantigen induction and proteins that regulate
lymphocyte homeostasis) include, without limitation, those

described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or

erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to

5   prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or

10   complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those

15   usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow

20   transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

      The activity of a protein of the invention may, among other means, be measured by the following methods:

25   Suitable assays for proliferation and

differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the

presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth

repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful

5   in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

10   Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue

15   is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to

20   tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the

25   repair of congenital, trauma induced, or other tendon or

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ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming

5   cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be

10   useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be

15   useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to

20   neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's,

25   Parkinson's disease, Huntington's disease, amyotrophic

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lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be

useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

5   A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, 10   among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, 15   neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year 20   Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are 25   characterized by their ability to inhibit the release of

follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of

5   the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the

10 protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United

15 States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

20   The activity of a protein of the invention may, among other means, be measured by the following methods:

    Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-

25 782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et

al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell

chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will
5   identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for
10   movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta
15   Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

20   Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such
25   as hemophilias) or to enhance coagulation and other

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hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions

5   resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity

10   include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15   Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without

20   limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their

25   ligands) and receptor/ligand pairs involved in antigen

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presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity

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may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly

(such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or cardiac cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other

nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Examples

        The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic procedures with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold

Spring Harbor Laboratory, 1989]. Unless otherwise stated, restriction enzymes and various modifying enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the

5   enzyme reactions were as described in the attached instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1)   Selection of cDNAs Encoding Proteins Having

10   Hydrophobic Domains

Human liver cDNA library (WO 98/21328) and human stomach cancer cDNA library (WO 98/21328), as well as the cDNA libraries constructed from human kidney mRNA (Clontech), human thymus mRNA (Clontech) and human umbilical cord blood

15   mRNA were used as cDNA libraries.

Full-length cDNA clones were selected from the respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The

20   hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a

25   hydrophobic domain. A clone that has a hydrophobic region

being assumed as a secretory signal or a transmembrane
domain in the amino acid sequence of the encoded protein was
selected as a clone candidate.

(2)   Protein Synthesis by In Vitro Translation

The plasmid vector bearing the cDNA of the present
invention was used for in vitro transcription/translation
with a $T_N T$ rabbit reticulocyte lysate kit (Promega). In this
case, [^{35}S]methionine was added to label the expression
product with a radioisotope. Each of the reactions was
carried out according to the protocols attached to the kit.
Two micrograms of the plasmid was subjected to the reaction
at 30°C for 90 minutes in the reaction solution of a total
volume of 25 µl containing 12.5 µl µ of $T_N T$ rabbit
reticulocyte lysate, 0.5 µl of a buffer solution (attached
to the kit), 2 µl of an amino acid mixture (without
methionine), 2 µl of [^{35}S]methionine (Amersham) (0.37 MBq/µl),
0.5 µl of T7 RNA polymerase, and 20 U of RNasin. The
experiment in the presence of a membrane system was carried
out by adding 2.5 µl of a canine pancreas microsome fraction
(Promega) to the reaction system. To 3 µl of the reaction
solution was added 2 µl of the SDS sampling buffer (125 mM
Tris-hydrochloride buffer, pH 6.8, 120 mM 2-mercaptoethanol,
2% SDS solution, 0.025% bromophenol blue and 20% glycerol)
and the resulting mixture was heated at 95°C for 3 minutes
and then subjected to SDS-polyacrylamide gel electrophoresis.

The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression in COS7

Escherichia coli cells harboring the expression vector for the protein of the present invention were cultured at 37°C for 2 hours in 2 ml of the 2 x YT culture medium containing 100 µg/ml of ampicillin, the helper phage M13KO7 (50 µ l) was added thereto, and the cells were then cultured at 37°C overnight. Single-stranded phage particles were obtained by polyethylene glycol precipitation from a supernatant separated by centrifugation. The particles were suspended in 100 µl of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from monkey kidney, COS7, were cultured at 37°C in the presence of 5% CO_2 in the Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal calf serum. 1 x 10^5 COS7 cells were inoculated into a 6-well plate (Nunc, well diameter: 3 cm) and cultured at 37°C for 22 hours in the presence of 5% CO_2. After the medium was removed, the cell surface was washed with a phosphate buffer solution followed by DMEM containing 50 mM Tris-hydrochloride (pH 7.5) (TDMEM). A suspension containing 1 µl of the single-stranded phage suspension, 0.6 ml of the DMEM medium and 3 µl of TRANSFECTAM™ (IBF) was added to the cells and the cells were cultured at 37°C for 3 hours in the presence of 5% CO_2. After the sample solution was removed,

the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the cells were cultured at 37°C for 2 days in the presence of 5% CO_2. After the medium was exchanged for a medium containing

5   [^{35}S]cysteine or [^{35}S]methionine, the cells were cultured for one hour. After the medium and the cells were separated each other by centrifugation, proteins in the medium fraction and the cell membrane fraction were subjected to SDS-PAGE.

(4)   Preparation of Antibodies

10   A plasmid vector containing the cDNA of the present invention was dissolved in a phosphate buffer solution (PBS: 145 mM NaCl, 2.68 mM KCl, 8.09 mM Na_2HPO_4, 2 mM KH_2PO_4, pH 7.2) to a concentration of 2 µg/µl. 25 µl each (a total of 50 µl) of the thus-prepared plasmid solution in

15   PBS was injected into the right and left musculi quadriceps femoris of three mice (ICR line) using a 26 guage needle. After similar injections were repeated for one month at intervals of one week, blood was collected. The collected blood was stored at 4°C overnight to coagulate the blood,

20   and then centrifuged at 8,000 x g for five minutes to obtain a supernatant. NaN_3 was added to the supernatant to a concentration of 0.01% and the mixture was then stored at 4°C. The generation of an antibody was confirmed by immunostaining of COS7 cells into which the corresponding

25   vector had been introduced or by Western blotting using a

58

cell lysate or a secreted product.

(5)   Clone Examples

<HP03171> (SEQ ID NOS: 1, 11 and 21)

Determination of the whole base sequence of the

5   cDNA insert of clone HP03171 obtained from cDNA library of

human thymus revealed the structure consisting of a 90-bp

5'-untranslated region, a 804-bp ORF, and a 1148-bp 3'-

untranslated region. The ORF encodes a protein consisting of

267 amino acid residues and there existed one putative

10   transmembrane domain. Figure 1 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro

translation resulted in formation of a translation product

of 34 kDa that was somewhat larger than the molecular weight

15   of 30,234 predicted from the ORF. In this case, the

addition of a microsome led to the formation of a product of

38 kDa. In addition, there exists in the amino acid sequence

of this protein one site at which N-glycosylation may occur

(Asn-Thr-Thr at position 169).

20   The search of the protein database using the amino

acid sequence of the present protein revealed that the

protein was similar to chicken putative transmembrane

protein E3-16 (Accession No. AAB70816). Table 3 shows the

comparison between amino acid sequences of the human protein

25   of the present invention (HP) and chicken putative

59

transmembrane protein E3-16 (GG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.0% in the entire region.

Table 3

HP MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGSSVGGVCY

   ***.**..*.*   . *.*......   .   .*.   *. *.. . ..   *.

GG MVKVSFNSALAH--KEAANKEEENSQVL-ILPPDAKEPEDVVVPAGHKRAWCWCM---CF

HP LSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLY-EDSL-----SSQVRTQM--

      .. . *......*.*.** ..*   . .* **. * **.*   ..*.....

GG ---GLAFMLAGVILGGAYLYKYFAFQQ--GGVYF-CGIKYIEDGLSLPESGAQLKSARYH

HP ELEEDVKIYLDENYERINVPVPQFGGGDPADIIHDFQRGLTAYHDISLDKCYVIELNTTI

   ..*....* .*. * *.****.*...*****.***.* **** *.******** ***..

GG TIEQNIQILEEEDVEFISVPVPEFADSDPADIVHDFHRRLTAYLDLSLDKCYVIPLNTSV

HP VLPPRNFWELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGKDTYRLRR

   *.**.** ***.*.* ******.*.*.*.*.**..... ..** ***.**.**.**.*.*

GG VMPPKNFLELLINIKAGTYLPQSYLIHEQMIVTDRIENVDQLGFFIYRLCRGKETYKLQR

25

HP RATRRRINKRGAKNCNAIRHFENTFVVETLICGVV

..... *.**.* **. ****** *..*****

GG KEAMKGIQKREAVNCRKIRHFENRFAMETLICEQ

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AL036384) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03424> (SEQ ID NOS: 2, 12 and 22)

Determination of the whole base sequence of the cDNA insert of clone HP03424 obtained from cDNA library of human liver revealed the structure consisting of a 4-bp 5'-untranslated region, a 1260-bp ORF, and a 169-bp 3'-untranslated region. The ORF encodes a protein consisting of 419 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was somewhat larger than the molecular weight

61

of 46,375 predicted from the ORF.   In this case, the
addition of a microsome led to the formation of a product of
54 kDa. In addition, there exist in the amino acid sequence
of this protein six sites at which N-glycosylation may occur
5   (Asn-Ala-Ser at position 29, Asn-Val-Thr at position 40,
Asn-Cys-Thr at position 112, Asn-Lys-Ser at position 135,
Asn-Ile-Ser at position 172 and Asn-Phe-Ser at position 189).
Application of the (-3,-1) rule, a method for predicting the
cleavage site of the secretory signal sequence, allows to
10   expect that the mature protein starts from aspartic acid at
position 28.

          The search of the protein database using the amino
acid sequence of the present protein revealed that the
protein was similar to Drosophila melanogaster GOLIATH
15   protein (Accession No. Q06003).   Table 4 shows the
comparison between amino acid sequences of the human protein
of the present invention (HP) and Drosophila melanogaster
GOLIATH protein (DM). Therein, the marks of -, *, and .
represent a gap, an amino acid residue identical with that
20   of the protein of the present invention, and an amino acid
residue similar to that of the protein of the present
invention, respectively. The both proteins shared a homology
of 40.8% in the intermediate region of 218 amino acid
residues.

25

Table 4

```
    HP MSCAGRAGPARLAALALLTCSLWPARADNASQEYYTALINVTVQEPGRGAPLTFRIDRGR


 5  HP YGLDSPKAEVRGQVLAPLPLHGVADHLGCDPQTRFFVPPNIKQWIALLQRGNCTFKEKIS


    HP RAAFHNAVAVVIYNNKSKEEPVTMTHPGTGDIIAVMITELRGKDILSYLEKNISVQMTIA
                              .* **.. .   *.*.    *.*. .* ..*
    DM                        MQLEKMQIKGKTRNIAAVITYQNIGQDLSLTLDKGYNVTISII

10
    HP VGTR--MPPKNFSRGSLVFVSISFIVLMIISSAWLIFYFIQKIRYTNARDRNQRRLGDAA
        * *  .. ...*.*..*******  *.   *****.**..** .*.*.. *.* ...
    DM EGRRGVRTISSLNRTSVLFVSISFIVDDIL--CWLIFYYIQRFRYMQAKDQQSRNLCSVT


15  HP KKAISKLTTRTVKKGDKETDPDFDHCAVCIESYKQNDVVRILPCKHVFHKSCVDPWLSEH
        **** *..*.* * .* *.* * * **.***.**..*..******* ***.*.**** **
    DM KKAIMKIPTKTGKFSD-EKDLDSDCCAICIEAYKPTDTIRILPCKHEFHKNCIDPWLIEH


    HP CTCPMCKLNILKALGIVPNLPCTDNVAFDMERLTRTQAVNRRSALGDLAGDNSLGLEPLR
20      *******..** * * ..  ...   .. ...... ...   . ...  *.**.
    DM RTCPMCKLDVLKFYGYVVGDQIYQTPS--PQHTAPIASIEEVPVIVVAVPHGPQPLQPLQ


    HP TSGISPLPQDGELTPRTGEINIAVTKEWFIIASFGLLSALTLCYMIIRATASLNANEVEW
        .*..*...
25  DM ASNMSSFAPSHYFQSSRSPSSSVQQQLAPLTYQPHPQQAASERGRRNSAPATMPHAITAS
```

HP F

DM HQVTDV

5   _____

        Furthermore, the search of the GenBank using the

base sequences of the present cDNA has revealed the

registration of sequences that shared a homology of 90% or

10   more (for example, Accession No. AA082118) among ESTs.

However, since they are partial sequences, it can not be

judged whether or not they encode the same protein as the

protein of the present invention.

        <HP03444> (SEQ ID NOS: 3, 13 and 23)

15   Determination of the whole base sequence of the

cDNA insert of clone HP03444 obtained from cDNA library of

human kidney revealed the structure consisting of a 209-bp

5'-untranslated region, a 1248-bp ORF, and a 460-bp 3'-

untranslated region. The ORF encodes a protein consisting of

20   415 amino acid residues and there existed a putative

secretory signal at the N-terminus. Figure 3 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro

translation resulted in formation of a translation product

25   of 43 kDa that was somewhat smaller than the molecular

64

weight of 45,691 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 42 kDa.   Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal

5   sequence, allows to expect that the mature protein starts from glutamine at position 24.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human type I procollagen C-proteinase

10   enhancer protein (Accession No. BAA23281).   Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human type I procollagen C-proteinase enhancer protein (CP). Therein, the marks of -, *, and . represent a gap, an amino acid residue

15   identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.6% in the entire region.

20   Table 5

HP   MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYP

        * **. * * .. .. .**** *** ..****...*****..**

CP MLPAATASLLGPLLTACALLPFA-Q-GQTPNYTRPVFLCGGDVKGESGYVASEGFPNLYP

25

```
    HP PNSKCTWKITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGH-ANGQRIGRFCGTFRPG
       **..*.*.******..* *.** .*** .  **** ..*..*  ..***.*********.
    CP PNKECIWTITVPEGQTVSLSFRVFDLELHPACRYDALEVFAGSGTSGQRLGRFCGTFRPA


 5  HP ALVSSGNKMMVQMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDR
       .**..**.. ..*..*.*.*.**.  .*. .... ..*.*** *... *...*****..
    CP PLVAPGNQVTLRMTTDEGTGGRGFLLWYSGRATSGTEHQFCGGRLEKAQGTLTTPNWPES


    HP DYPAGVTCVWHIVAPKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGD
10     ***.*..* ***.** .*.*.*.*****.*.*.***** *.****.  .*.**.**.***
    CP DYPPGISCSWHIIAPPDQVIALTFEKFDLEPDTYCRYDSVSVFNGAVSDDSRRLGKFCGD


    HP SPPAPIVSERNELLIQFLSDLSLTADGFIGHYIFRPKKLPTTTE----------------
       . *..* ** ****.**.****.***** . *    *.  .....
15  CP AVPGSISSEGNELLVQFVSDLSVTADGFSASYKTLPRGTAKEGQGPGPKRGTEPKVKLPP


    HP QPVTTTFPVTTGLKTTVALCQQKCRRTGTLEGNYCSSDFVLAGTVITTITRDG-SLHATV
       .. ... . ..    .... *...*******..*.*.*..*...**  .   * .* .**
    CP KSQPPEKTEESPSAPDAPTCPKQCRRTGTLQSNFCASSLVVTATVKSMVREPGEGLAVTV

20
    HP SIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRRGLNYIIMGQVGEDGRGKIM-PNSF
       *.*. **.*.*.. . .. * .. * ***** ...*..*..**** *..** .. *.**
    CP SLIGAYKTGGLDLPSPPTGASLKFYVPCKQCPPMKKGVSYLLMGQV-EENRGPVLPPESF


25  HP IMMFKTKNQKLLDALKNKQC
```

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... ........*..*....*
```

CP VVLHRPNQDQILTNLSKRKCPSQPVRAAASQD

---

5   The search of the GenBank using the base sequences

of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example,

Accession No. D78874) among ESTs. However, since they are

partial sequences, it can not be judged whether or not they

10   encode the same protein as the protein of the present

invention.

           <HP03478> (SEQ ID NOS: 4, 14 and 24)

           Determination of the whole base sequence of the

cDNA insert of clone HP03478 obtained from cDNA library of

15   human umbilical cord blood revealed the structure consisting

of a 224-bp 5'-untranslated region, a 1143-bp ORF, and a

891-bp 3'-untranslated region. The ORF encodes a protein

consisting of 380 amino acid residues and there existed five

putative transmembrane domains. Figure 4 depicts the

20   hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein.   In vitro

translation resulted in formation of a translation product

of high molecular weight.

           The search of the protein database using the amino

25   acid sequence of the present protein revealed that the

protein was similar to Halocynthia roretzi HrPET-1 protein

(Accession No. BAA81907).   Table 6 shows the comparison

between amino acid sequences of the human protein of the

present invention (HP) and Halocynthia roretzi HrPET-1

5   protein (HR). Therein, the marks of -, *, and . represent a

gap, an amino acid residue identical with that of the

protein of the present invention, and an amino acid residue

similar to that of the protein of the present invention,

respectively. The both proteins shared a homology of 36.8%

10   in the entire region.

Table 6

HP   MLQTLYDYFWWERLWLPVNLTWADLEDRDGRVYAKASDLYITLPLALLFLIVRYFFEL

15   .* .**..** *...*** ****.**.   ... .**..*.** . * .*. *

HR MDLLMDLYHWFWNEKFWLPQNLTWEDLKRTEEKQFGETRDLWLTFPLCITVLCIRFSVEK

HP YVATPLAALLNIKEKTRLRAPPNATLEHFYLTSGKQPKQVEVELLSRQSGLSGRQVERWF

        .* **. **..*. . ... * .**. * * ...*. .** *..*.* . .... **

20 HR GIARPLGKWLNLSERLHTPPRENIVLEKVYKTITRKPNYSQVEDLCKQTGWRKHEINVWF

HP RRRRNQDRPSLLKKFREASWRFTFYLIAFIAGMAVIVDKPWFYDMKKVWEGYPIQSTIPS

        *... .**. *.**.*. ***.***..*. *. *. *.   ...* ...** . ...

HR RKKNLVGRPTTLTKFQETFWRFAFYLTSFFYGLYVMYDQECVWQTEKCFSNYPEDHVLSQ

25

```
HP  Q-YWYYMIELSFYWSLLFSIASDVKRKDFKEQIIHHVATIILISFSWFANYIRAGTLIMA
    . *.**.***.**  .  ..     ******* * .***..****.. *.  **.. *..*..
HR  KIYYYYLIELAFYSATTLTQFFDVKRKDFWEMFIHHIVTIILLCGSYTLNYTKMGAFILV
```

```
HP  LHDSSDYLLESAKMFNYAGWKNTCNNIFIVFAIVFIITRLVILPFWILHCTLVYPLELYP
    .***.*. .* *** .**. . . * ** *.* *...******.**....  *.   *
HR  VHDSADFYIEFAKMGKYANNSLVTNVGFISFTISFFLSRLVILPLWIVPSIWFYGIYTYN
```

```
HP  AFFGYYFFNSMMGVLQLLHIFWAYLILRMAHKFITGKLVEDERSDREETESSEGEEAAAG
    .. ..* ... .*****..*   *.. *. *   ..* . .. .*..*.*.*.*  .
HR  CAMA-WLFCALL-ILQLLHFYWFSHIVKAAYASILVGVIERDTRSESEDSSAEDETAKYS
```

```
HP  GGAKSRPLANGHPILNNNHRKND
    *.
HR  VGSGDYTESNGIHKRVVTAR
```

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T27334) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03499> (SEQ ID NOS: 5, 15 and 25)

Determination of the whole base sequence of the cDNA insert of clone HP03499 obtained from cDNA library of human kidney revealed the structure consisting of a 129-bp 5'-untranslated region, a 1758-bp ORF, and a 86-bp 3'-

5   untranslated region. The ORF encodes a protein consisting of 585 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro

10   translation resulted in formation of a translation product of 63 kDa that was almost identical with the molecular weight of 63,987 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 82 kDa. In addition, there exist in the amino acid sequence

15   of this protein five sites at which N-glycosylation may occur (Asn-Ile-Thr at position 89, Asn-Glu-Thr at position 106, Asn-Ala-Thr at position 189, Asn-Arg-Thr at position 220 and Asn-Ala-Thr at position 315).

The search of the protein database using the amino

20   acid sequence of the present protein revealed that the protein was similar to Chinese hamster hypothetical protein 2BE2121 (Accession No. A30227). Table 7 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Chinese hamster

25   hypothetical protein 2BE2121 (CH). Therein, the marks of -,

70

*, and . represent a gap, an amino acid residue identical

with that of the protein of the present invention, and an

amino acid residue similar to that of the protein of the

present invention, respectively. The both proteins shared a

5   homology of 44.8% in the entire region.

Table 7

HP MVCREQLSKNQVKWVFAGITCVSVVVIAAIVLAITLRRPGCELEACSPDADMLDYLLSLG

10   ..***.*. .

CH   SWSENILDYFLRNS

HP QISRRDALEVTWYHAANSKKAMTAALNSNITVLEADVNVEGLGTANETGVPIMAHPPTIY

    . *. *..**** *..* .**.*. ..****. . ...* * *******..

15 CH QITTEDGAEIIWYHAANHKSQMQEALRSAAHMIEADVLLPS--DGSEHGQPIMAHPPEMN

HP SDNTLEQWLDAVLGSSQKGIKLDFKNIKAVGPSLDLLRQLTEEGKVRRPIWINADILKGP

    *****..**..*. .*.********.. *. .*. .* .... *.*.***.* **

CH SDNTLQEWLAEVM-KSNKGIKLDFKSLAAARASMLFLDNVKQH--LQCPVWMNADVLPGP

20

HP NMLISTEVNATQFLALVQEKYPKATLSPGWTTFYMSTSPNRTYTQAMVEKMHELVGGVPQ

    *   *. *.*..**. * . .*..*.* ****. ... * .*. .**..*. ..*..*

CH NG-SSKVVDAKAFLDTVTSFFPDVTFSLGWTTGWHPEKVNEGYSWTMVKEMDYICSGLTQ

25 HP RVTFPVRSSMVRAAWPHFSWLLSQSERYSLTLWQAASDPMSVEDLLYVRDNTAVHQVYYD

71

```
     .******...**..  ...  ***..*.*****.* . .*. ..*****.**  .  **.**
CH  PVTFPVRAALVRQSCSQLLWLLKKSNRYSLTVWTGKDDSYPTEDLLYIRDYFNKTQVFYD


HP  IFEPLLSQFKQLALNATRKPMYYTGGSLIPLLQLPGDDGLNVEWLVPDVQGSGKTATMTL

     *.**  .***
CH  ILEPQSHEFKQAIGI
```

 5

_____

        Furthermore, the search of the GenBank using the

10 base sequences of the present cDNA has revealed the

    registration of sequences that shared a homology of 90% or

    more (for example, Accession No. R92398) among ESTs. However,

    since they are partial sequences, it can not be judged

    whether or not they encode the same protein as the protein

15 of the present invention.

        <HP03500> (SEQ ID NOS: 6, 16 and 26)

        Determination of the whole base sequence of the

    cDNA insert of clone HP03500 obtained from cDNA library of

    human kidney revealed the structure consisting of a 134-bp

20 5'-untranslated region, a 996-bp ORF, and a 476-bp 3'-

    untranslated region. The ORF encodes a protein consisting of

    331 amino acid residues and there existed one putative

    transmembrane domain at the N-terminus. Figure 6 depicts the

    hydrophobicity/hydrophilicity profile, obtained by the Kyte-

25 Doolittle method, of the present protein. In vitro

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translation resulted in formation of a translation product of 38 kDa that was almost identical with the molecular weight of 37,694 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the amino acid sequence of the protein matched with that of human hypothetical protein (Accession No. AAC05803) in which a region of 62 amino acid residues from glycine at position 88 to lysine at position 149 was deleted.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA340631) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10691> (SEQ ID NOS: 7, 17 and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10691 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 246-bp 5'-untranslated region, a 1038-bp ORF, and a 1096-bp 3'-untranslated region. The ORF encodes a protein consisting of 345 amino acid residues and there existed at least two putative transmembrane domains. Figure 7 depicts the hydrophobicity/hydrophilicity profile, obtained by the

73

Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human BB1 protein (Accession No. AAB37433). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human BB1 protein (BB). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The C-terminal region of 215 amino acid residues of the present protein shared a homology of 81.9% with the N-terminal region of human BB1 protein.

Table 8

HP MSPEEWTYLVVLLISIPIGFLFKKAGPGLKRWGAAAVGLGLTLFTCGPHTLHSLVTILGT

HP WALIQAQPCSCHALALAWTFSYLLFFRALSLLGLPTPTPFTNAVQLLLTLKLVSLASEVQ

HP DLHLAQRKEMASGFSKGPTLGLLPDVPSLMETLSYSYCYVGIMTGPFFRYRTYLDWLEQP
                    *************. . .*   . * . * .. .   .
BB   MASGFSKGPTLGLLRRALPDGDT-QLQLLLRGNHDRPVLPLPHLPGLAGAA

HP FPGAVPSLRPLLRRAWPAPLFGLLFLLSSHLFPLEAVREDAFYARPLPARLFYMIPVFFA

   .*. .**

BB LPRGSASLRPLLRRAWPAPLFGLLFLLSSHLFPLEAVREDAFYARPLPARLFYMIPVFFA

5

HP FRMRFYVAWIAAECGCIAAGFGAYPVAAKARAGGGPTLQCPPPSSPEKAASLEYDYETIR

   ****

BB FRMRFYVAWIAAECGCIAAGFGAYPVAAKARAGGGPTLQCPPPSSPEKAASLEYDYETIR

10 HP NIDCYSTDFCVRVRDGMRYWNMTVQWWLAQYIYKSAPARSYVLRL

      ****

    BB NIDCYSTDFCVRVRDGMRYWNMTVQWWLAQYIYKSAPARSYVLRTAWTMLLSAYWHGLHP

_____

15   The search of the GenBank using the base sequences

    of the present cDNA has revealed the registration of

    sequences that shared a homology of 90% or more (for example,

    Accession No. W48653) among ESTs. However, since they are

    partial sequences, it can not be judged whether or not they

20 encode the same protein as the protein of the present

    invention.

          <HP10703> (SEQ ID NOS: 8, 18 and 28)

          Determination of the whole base sequence of the

    cDNA insert of clone HP10703 obtained from cDNA library of

25 human kidney revealed the structure consisting of a 359-bp

5'-untranslated region, a 270-bp ORF, and a 1388-bp 3'-untranslated region. The ORF encodes a protein consisting of 89 amino acid residues and there existed one putative transmembrane domain. Figure 8 depicts the

5   hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 18 kDa that was larger than the molecular weight of 10,469 predicted from the ORF.

10   The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T08343) among ESTs. However, since they are partial sequences, it can not be judged whether or not they

15   encode the same protein as the protein of the present invention.

        <HP10711> (SEQ ID NOS: 9, 19 and 29)

        Determination of the whole base sequence of the cDNA insert of clone HP10711 obtained from cDNA library of

20   human kidney revealed the structure consisting of a 29-bp 5'-untranslated region, a 1221-bp ORF, and a 356-bp 3'-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative

25   transmembrane domain at the N-terminus. Figure 9 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 44 kDa that was almost identical with the molecular

5   weight of 43,836 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 58 kDa. In addition, there exist in the amino acid sequence of this protein seven sites at which N-glycosylation may occur (Asn-Ser-Thr at position 65, Asn-Trp-Ser at position

10   95, Asn-Val-Ser at position 134, Asn-Ile-Thr at position 159, Asn-Gly-Ser at position 187, Asn-Arg-Ser at position 230 and Asn-Leu-Thr at position 333). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature

15   protein starts from glutamic acid at position 36.

        The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse kidney predominant protein (Accession No. BAA92527). Table 9 shows the comparison

20   between amino acid sequences of the human protein of the present invention (HP) and mouse kidney predominant protein (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

25   of the protein of the present invention, respectively. The

both proteins shared a homology of 79.9% in the entire region.

Table 9

5   _____

HS MRGSVECTWGWGHCAPSPLLLWTLLLFAAPFGLLGEKTRQVSLEVIPNWLGPLQNLLHIR

   *   *** .***.* ** .**. .***** **.*****.***..* .* *******

MM MFRCWGPHWGWVPCAPTPWLLLSLLVCSAPFGLQGEETRQVSMEVISGWPNP-QNLLHIR

10 HS AVGTNSTLHYVWSSLGPLAVVMVATNTPHSTLSVNWSLLLSPEPDGGLMVLPKDSIQFSS

   .********** ***.*****..*.***********.*.*.******.******

MM AVGSNSTLHYVWSSLGPPAVVLVATNTTQSVLSVNWSLLLSPDPAGALMVLPKSSIQFSS

HS ALVFTRLLEFDSTNVSDTAAKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHPMND

15 ************** .*. .*.* *.********.*******.*** *.***.***.*..*

MM ALVFTRLLEFDSTNASE-GAQPPGKPYPPYSLAKFSWNNITNSLDLANLSADFQGRPVDD

HS PTRTFANGSLAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLFGLEVAT

   ** .******.*.*******.**************.*******.*******.*********

20 MM PTGAFANGSLTFKVQAFSRSGRPAQPPRLLHTADVCQLEVALVGASPRGNHSLFGLEVAT

HS LGQGPDCPSMQEQHSIDDEYAPAVFQLDQLLWGSLPSGFAQWRPVAYSQKPGGRESALPC

   *********..*..*************.****** **** ******.*.. .*******

MM LGQGPDCPSVNERNSIDDEYAPAVFQLNQLLWGSSPSGFMQWRPVAFSEEERARESALPC

25

HS QASPLHPALAYSLPQSPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGF

    .**..** ***.*.******************.********.**.******.**

MM QASTLHSTLASSLPHSPIVQAFFGSQNNFCAFNLTFGAPTGPGYWDQYYLCWSMLLGMGF

5   HS PPVDGLSPLVLGIMAVALGAPGLMLLGGGLVLLLHHKKYSEYQSIN

    **** .*****************.***** ***.*..*******

MM PPVDIFSPLVLGIMAVALGAPGLMFLGGGLFLLLRHRRYSEYQSIN

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10   The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. AA362394) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
15   encode the same protein as the protein of the present
invention.

    <HP10712> (SEQ ID NOS: 10, 20 and 30)

    Determination of the whole base sequence of the
cDNA insert of clone HP10712 obtained from cDNA library of
20   human kidney revealed the structure consisting of a 52-bp
5'-untranslated region, a 579-bp ORF, and a 1064-bp 3'-
untranslated region. The ORF encodes a protein consisting of
192 amino acid residues and there existed four putative
transmembrane domains. Figure 10 depicts the
25   hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of high molecular weight.

　　The search of the protein database using the amino
5　acid sequence of the present protein revealed that the
protein was similar to mouse calcium channel gamma 5 subunit
(Accession No. CAB86387). Table 10 shows the comparison
between amino acid sequences of the human protein of the
present invention (HP) and mouse calcium channel gamma 5
10　subunit (MM). Therein, the marks of -, *, and . represent a
gap, an amino acid residue identical with that of the
protein of the present invention, and an amino acid residue
similar to that of the protein of the present invention,
respectively. The both proteins shared a homology of 75.0%
15　in the entire region.

Table 10

HS MTAVGVQAQRPLGQRQPRRSFFESFIRTLIITCVALAVVLSSVSICDGHWLLAEDRLFGL

20　　***.*.**.. ** ..*.*************.*.******************.**.****

MM MTAIGAQAHKLLGLKRPHRSFFESFIRTLIIVCTALAVVLSSVSICDGHWLLVEDHLFGL

HS WHFCTTTNQSVPICFRDLGQAHVPGLAVGMGLVRSVGALAVVAAIFGLEFLMVSQLCEDK

　　*.***..*.* * *.***.***.*********.***.*.**********.*.***.***

25　MM WYFCTIGNHSEPHCLRDLSQAHMPGLAVGMGLARSVAAMAVVAAIFGLEMLIVSQVCEDV

HS HSQCKWVMGSILLLVSFVLSSGGLLGFVILLRNQVTLIGFTLMFWCEFTASFLLFLNAIS

    .*. **..** ****.*.*******.*.***.**..*.***************.**** *

MM RSRRKWAIGSYLLLVAFILSSGGLLTFIILLKNQINLLGFTLMFWCEFTASFLFFLNAAS

HS GLHINSITHPWE

    ******.*.**.

MM GLHINSLTQPWDPPAGTLAYRKRGYDGTSLI

        Furthermore, the search of the GenBank using the
base sequences of the present cDNA has revealed the
registration of sequences that shared a homology of 90% or
more (for example, Accession No. AA910339) among ESTs.
However, since they are partial sequences, it can not be
judged whether or not they encode the same protein as the
protein of the present invention.

        <HP03010> (SEQ ID NOS: 31, 41 and 51)

        Determination of the whole base sequence of the
cDNA insert of clone HP03010 obtained from cDNA library of
human kidney revealed the structure consisting of a 97-bp
5'-untranslated region, a 1134-bp ORF, and a 320-bp 3'-
untranslated region. The ORF encodes a protein consisting of
377 amino acid residues and there existed at least eight
putative transmembrane domains. Figure 11 depicts the

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hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 42 kDa that was almost identical with the molecular

5   weight of 41,462 predicted from the ORF as well as a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Arabidopsis thaliana hypothetical

10   protein (Accession No. AAC34490). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Arabidopsis thaliana hypothetical protein (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that

15   of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 42.0% in the entire region other than the N-terminal region.

20

Table 11

HP MDSALSDPHNGSAEAGGPTNSTTRPPSTPEGIALAYGSLLLMALLPIFFGALRSVRCARG

                                                          * * *.

25   AT   MKNCERFANLALAGLTLAPLVVRVNPNLNVILTACITVYVGCFRS

```
HP  KNASDMPETITSRDAARFPIIASCTLLGLYLFFKIFSQEYINLLLSMYFFVLGILALSHT

    ...  .**... .* ***...* **.*.*.**..*.. .* .*. *******.*** *

AT  VKDTPPTETMSKEHAMRFPLVGSAMLLSLFLLFKFLSKDLVNAVLTAYFFVLGIVALSAT
```

5

```
HP  ISPFMNKFFPASFPNRQYQLLFTQGSGENKEEIINYEFDTKDLVCLGLSSIVGVWYLLRK

    . * ...*.*... ..       *         . .. **.....*   ... .** .*

AT  LLPAIRRFLPNPWNDNLIVWRF------PYFKSLEVEFTKSQVVAGIPGTFFCAWYAWKK
```

10

```
HP  HWIANNLFGLAFSLNGVELLHLNNVSTGCILLGGLFIYDVFWVFGTNVMVTVAKSFEAPI

    **.***..**.*...*.*.* *.. .** ***.***.**.**** * ***.*****.***

AT  HWLANNILGLSFCIQGIEMLSLGSFKTGAILLAGLFFYDIFWVFFTPVMVSVAKSFDAPI
```

```
HP  KLVFPQDLLEKGLEANNFAMLGLGDVVIPGIFIALLLRFDISLKKNTHTYFYTSFAAYIF
```

15

```
    **.** .   ..* . ..******.******.** ****.* ..... ** ..* .*

AT  KLLFPTG---DALRP--YSMLGLGDIVIPGIFVALALRFDVSRRRQPQ-YFTSAFIGYAV
```

```
HP  GLGLTIFIMHIFKHAQPALLYLVPACIGFPVLVALAKGEVTEMFSYEESNPKDPAAVTES

    *. *** .*. *. *******.*** *** .   . .*... .....**.... *...**
```

20

```
AT  GVILTIVVMNWFQAAQPALLYIVPAVIGFLASHCIWNGDIKPLLAFDESKTEE-ATTDES
```

```
HP  KEGTEASASKGLEKKEK

    *...*.. ...

AT  KTSEEVNKAHDE
```

25 _____

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or

5   more (for example, Accession No. AA380429) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03576> (SEQ ID NOS: 32, 42 and 52)

10   Determination of the whole base sequence of the cDNA insert of clone HP03576 obtained from cDNA library of human kidney revealed the structure consisting of a 88-bp 5'-untranslated region, a 246-bp ORF, and a 1379-bp 3'-untranslated region. The ORF encodes a protein consisting of

15   81 amino acid residues and there existed two putative transmembrane domains. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product

20   of 20 kDa that was larger than the molecular weight of 9,178 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human vacuolar proton ATPase 9 kDa

25   (Accession No. NP_003936). Table 12 shows the comparison

between amino acid sequences of the human protein of the
present invention (HP) and human vacuolar proton ATPase 9
kDa (VP). Therein, the marks of -, *, and . represent a gap,
an amino acid residue identical with that of the protein of
5   the present invention, and an amino acid residue similar to
that of the protein of the present invention, respectively.
The both proteins shared a homology of 71.2% in the entire
region.

10   Table 12

HP MTAHSFALPVIIFTTFWGLVGIAGPWFVPKGPNRGVIITMLVATAVCCYLFWLIAILAQL

   *. *....*.*....***.**.   ***.*************. .***************

VP MAYHGLTVPLIVMSVFWGFVGFLVPWFIPKGPNRGVIITMLVTCSVCCYLFWLIAILAQL

15

HP NPLFGPQLKNETIWYVRFLWE

   ***************... *

VP NPLFGPQLKNETIWYLKYHWP

20

        Furthermore, the search of the GenBank using the
base sequences of the present cDNA has revealed the
registration of sequences that shared a homology of 90% or
more (for example, Accession No. W22566) among ESTs. However,
25   since they are partial sequences, it can not be judged

whether or not they encode the same protein as the protein of the present invention.

<HP03611> (SEQ ID NOS: 33, 43 and 53)

Determination of the whole base sequence of the

5   cDNA insert of clone HP03611 obtained from cDNA library of human kidney revealed the structure consisting of a 189-bp 5'-untranslated region, a 1464-bp ORF, and a 105-bp 3'-untranslated region. The ORF encodes a protein consisting of 487 amino acid residues and there existed eleven putative

10   transmembrane domains. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

15   The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human cystine/glutamate transporter (Accession No. BAA82628). Table 13 shows the comparison between amino acid sequences of the human protein of the

20   present invention (HP) and human cystine/glutamate transporter (CG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present

25   invention, respectively. The both proteins shared a homology

of 43.8% in the entire region other than the N-terminal
region.

Table 13

5   _____

HP   MGDTGLRKRREDEKSIQSQEPKTTSLQKELGLISGISIIVGTIIGS

                .... *.....*..*.***.*****.

CG MVRKPVVSTISKGGYLQGNVNGRLPSLGNKEPPGQEKVQLKRKVTLLRGVSIIIGTIIGA

10   HP GIFVSPKSVLSNTEAVGPCLIIWAACGVLATLGALCFAELGTMITKSGGEYPYLMEAYGP

        ..** **..** .*.**..****. .***..***** *.****.*.*..*..**

     CG GIFISPKGVLQNTGSVGMSLTIWTVCGVLSLFGALSYAELGTTIKKSGGHYTYILEVFGP

     HP IPAYLFSWASLIVIKPTSFAIICLSFSEYVCAPFYVGCKPPQIVVKCLAAAAILFISTVN

15   .**.. *..*..*.*.. *.*.*.*. *. .**.. *. *....* ..*..* . ..*

     CG LPAFVRVWVELLIIRPAATAVISLAFGRYILEPFFIQCEIPELAIKLITAVGITVVMVLN

     HP SLSVRLGSYVQNIFTAAKLVIVAIIIISGLVLLAQGNTKNFDNSFEGAQLSVGAISLAFY

        *.**. .. .*..* **. . ***..*.. * .*.*.**...*.* . *.. ..****

20   CG SMSVSWSARIQIFLTFCKLTAILIIIVPGVMQLIKGQTQNFKDAFSGRDSSITRLPLAFY

     HP NGLWAYDGWNQLNYITEELRNPYRNLPLAIIIGIPLVTACYILMNVSYFTVMTATELLQS

        *..**.** **..***. ** ...**** *....** *.* **.***...*.*** *

     CG YGMYAYAGWFYLNFVTEEVENPEKTIPLAICISMAIVTIGYVLTNVAYFTTINAEELLLS

25

HP QAVAVTFGDRVLYPASWIVPLFVAFSTIGAANGTCFTAGRLIYVAGREGHMLKVLSYISV

    .******..*.*   * **.***.* .*. **. *...**.***.****. ..** * *

CG NAVAVTFSERLLGNFSLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV

5   HP RRLTPAPAIIFYGIIATIYIIPGDINSLVNYFSFAAWLFYGLTILGLIVMRFTRKELERP

    *. ** **.*   .. * ...**..**.*..*** *** **.. *** .*.. ...**

CG RKHTPLPAVIVLHPLTMIMLFSGDLDSLLNFLSFARWLFIGLAVAGLIYLRYKCPDMHRP

HP IKVPVVIPVLMTLISVFLVLAPIISKPTWEYLYCVLFILSGLLFYFLFVHY--KFGWAQK

10   .***. **.*......*.* .. *.* ..   ...*.*. *.**. . * * .

CG FKVPLFIPALFSFTCLFMVALSLYSDP-FSTGIGFVITLTGVPAYYLFIIWDKKPRWFRI

HP ISKPITMHLQMLMEVVPPEEDPE

    .*. **. **...**** *.

15 CG MSEKITRTLQIILEVVPEEDKL

The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
20 sequences that shared a homology of 90% or more (for example,
Accession No. R07056) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
encode the same protein as the protein of the present
invention.
25   <HP03612> (SEQ ID NOS: 34, 44 and 54)

Determination of the whole base sequence of the cDNA insert of clone HP03612 obtained from cDNA library of human kidney revealed the structure consisting of a 153-bp 5'-untranslated region, a 1128-bp ORF, and a 269-bp 3'-

5   untranslated region. The ORF encodes a protein consisting of 375 amino acid residues and there existed seven putative transmembrane domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro

10   translation resulted in formation of a translation product of 39 kDa that was somewhat larger than the molecular weight of 37,930 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the

15   protein was similar to human monocarboxylate transporter (Accession No. AAC70919). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human monocarboxylate transporter (MC). Therein, the marks of -, *, and . represent a gap, an

20   amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.7% in the N-terminal region of 192 amino acid residues.

25

Table 14

_____

HP   MTPQPAGPPDGGWGWVVAAAAFAINGLSYGLLRSLGLAFPDLAEHFDRSAQDTAW

      .*.   ********.*..*.*   *.**.. ..... * .... *. . ..**

MC MPPMPSAPPVHPPPDGGWGWIVVGATFISIGFSYAFPKAVTVFFKEIQQIFHTTYSEIAW

HP ISALALAVQQAASPVGSALSTRWGARPVVMVGGVLASLGFVFSAFASGLLHLYLGLGLLA

   .. * *..**.*.* ...*.****..**.* .**.*...*.*....***..*...

MC ISSIMLAVMYAGGPVSSVLVNKYGSRPVVIAGGLLCCLGMVLASFSSSVVQLYLTMGFIT

HP GFGWALVFAPALGTLSRYFSRRRVLAVGLALTGNGASSLLLAPALQLLLDTFGWRGALLL

   . *. ..***....** *.* .* ***..** .   *** * *..****.*..*.

MC GLGLAFNLQPALTIIGKYFYRKRPMANGLAMAGNPVFLSSLAPFNQYLFNTFGWKGSFLI

HP LGAITLHLTPCGALLLPLVLPGDPPAPPRSPLAALGLSLFTRRAFSIFALGTALVGGGYF

   **.. *.   *.*. **

MC LGSLLLNACVAGSLMRPLGPNQTTSKSKNKTGKTEDDSSPKKIKTKKSTWEKVNKYLDFS

HP VPYVHLAPRFRPGPGGIRSSAGGGRGCDGGCGRPAGLRVAGRPRLGAPPAAAGRIRGSDW

MC LFKHRGFLIYLSGNVIMFLGFFAPIIFPAPYAKDQGIDEYSAAFLLSVMAFVDMFARPSV

HP AGAVGGGAGARGGRRRELGGSPAGRGCGLWAERGELRPAGFRCTPRAGGRRRCGAGHRAG

MC GLIANSKYIRPRIQYFFSFAIMFNGVCHLLCPLAQDYTSLVLYAVFFGLGFGSVSSVLFE

HP DDADEPRGAPGPSPVRLPKG

MC TLMDLVGAPRFSSAVGLVTIVECGPVLLGPPLAGKLVDLTGEYKYMYMSCGAIVVAASVW

5   ——

        The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
10   Accession No. AI742291) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
encode the same protein as the protein of the present
invention.

        <HP10407> (SEQ ID NOS: 35, 45 and 55)

15   Determination of the whole base sequence of the
cDNA insert of clone HP10407 obtained from cDNA library of
human stomach cancer revealed the structure consisting of a
100-bp 5'-untranslated region, a 1053-bp ORF, and a 332-bp
3'-untranslated region. The ORF encodes a protein consisting
20   of 350 amino acid residues and there existed at least four
putative transmembrane domains. Figure 15 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein.

        The search of the protein database using the amino
25   acid sequence of the present protein revealed that the

protein was longer by 35 amino acid residues at the N-terminus than human hypothetical protein (Accession No. CAB43375).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of a clone beginning from the 117th base of the present cDNA (Accession No. AL050274).

<HP10713> (SEQ ID NOS: 36, 46 and 56)

Determination of the whole base sequence of the cDNA insert of clone HP10713 obtained from cDNA library of human kidney revealed the structure consisting of a 79-bp 5'-untranslated region, a 2004-bp ORF, and a 611-bp 3'-untranslated region. The ORF encodes a protein consisting of 667 amino acid residues and there existed nine putative transmembrane domains. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse retinoic acid-responsive protein (Accession No. AAC16016). Table 15 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse retinoic acid-

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responsive protein (MM). Therein, the marks of -, *, and .

represent a gap, an amino acid residue identical with that

of the protein of the present invention, and an amino acid

residue similar to that of the protein of the present

5   invention, respectively. The both proteins shared a homology

of 74.1% in the entire region.

Table 15

_____

10   HP   MSSQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLAS

               *.***.*.*.***   ****.** *.**.**** .* *. . **.* ******

     MM MESQASENGSQTSSGVTDDYS--SWYIEEPLGAEEVQPEGVIPLCQLTAPPALLHACLAS

     HP LSILVLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLL

15   **.*******.*****.*** * .   ************ ...******.**.*.*****

     MM LSFLVLLLLALLVRRRRLWPRCGHRGLGLPSPVDFLAGDLSWTVPAAVFVVLFSNLCLLL

     HP PDEDALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGST

               ..*.*..*.*.**. *..**.**.*.*.**.*********.*** ** ***..

20   MM PDENPLPFLNLTAASSPDGEMETSRGPWKLLALLYYPALYYPLAACASAGHQAAFLLGTV

     HP LSWAHLGVQVWQRAECPQVPKIYKYYSLLASLPLLLGLGFLSLWYPVQLVRSFSRRTGAG

               *****.******.***** *****.*********************.*...*****

     MM LSWAHFGVQVWQKAECPQDPKIYKHYSLLASLPLLLGLGFLSLWYPVQLVQSLRHRTGAG

25

HP SKGLQSSYSEEYLRNLLCRKKLGSSYH-TSKHGFLSWARVCLRHCIYTPQPGFHLPLKLV

    *.***.****.***.***.***.*. * .**...**.*.. .*.********.******

MM SQGLQTSYSEKYLRTLLCPKKLDSCSHPASKRSLLSRAWAFSHHSIYTPQPGFRLPLKLV

5   HP LSATLTGTAIYQVALLLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVELVKH

    .*******.*********.****.******..*****************.*********

MM ISATLTGTATYQVALLLLVSVVPTVQKVRAGINTDVSYLLAGFGIVLSEDRQEVVELVKH

HP HLWALEVCYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAI

10 ***..*.********** ***.*.*** ***.**.**********.* .* *******

MM HLWTVEACYISALVLSCASTFLLLIRSLRTHRANLQALHRGAALDLDPPLQSIHPSRQAI

HP FCWMSFSAYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWL

    .****.****** *******.*******.*****..*.********.*****.*****

15 MM VSWMSFCAYQTAFSCLGLLVQQVIFFLGTTSLAFLVFVPLLHGRNLLLLRSLESTWPFWL

HP TLALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSA

    *.********.**.*.** **.*.*.*****.*..*******.*.****..*.****.*.

MM TVALAVILQNIAANWIFLRTHHGYPELTNRRMLCVATFLLFPINMLVGAIMAVWRVLISS

20

HP LYNAIHLGQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPR

    ..********.***.*****.**.***.**.*****...***.***.*.* **

MM LYNTVHLGQMDLSLLPQRAASLDPGYHTYQNFLRIEASQSHPGVIAFCALLLHAPSPQPR

25 HP TMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKT

```
        .   ********.**.********* ***** . .*..**************.**.***.

MM PPLAPQDSLRPAEEEEGMQLLQTKDLMAKGAGHKGSQSRARWGLAYTLLHNPSLQAFRKA


HP ALLGANGAQP

   ** .*..

MM ALTSAKANGTQP
```

The search of the GenBank using the base sequences

of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example,

Accession No. AI760170) among ESTs. However, since they are

partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present

invention.

<HP10714> (SEQ ID NOS: 37, 47 and 57)

Determination of the whole base sequence of the

cDNA insert of clone HP10714 obtained from cDNA library of

human umbilical cord blood revealed the structure consisting

of a 82-bp 5'-untranslated region, a 1395-bp ORF, and a

1820-bp 3'-untranslated region. The ORF encodes a protein

consisting of 464 amino acid residues and there existed a

putative secretory signal at the N-terminus. Figure 17

depicts the hydrophobicity/hydrophilicity profile, obtained

by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 49 kDa that was somewhat smaller than the molecular weight of 52,340 predicted from the ORF. In this case, the addition of a microsome led to the formation of a

5 product of 52 kDa. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Ala-Thr at position 164 and Asn-Asp-Ser at position 320). Application of the (-3,-1) rule, a method for predicting the cleavage site of the

10 secretory signal sequence, allows to expect that the mature protein starts from threonine at position 22.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example,

15 Accession No. AA861134) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10716> (SEQ ID NOS: 38, 48 and 58)

20 Determination of the whole base sequence of the cDNA insert of clone HP10716 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 60-bp 5'-untranslated region, a 1413-bp ORF, and a 653-bp 3'-untranslated region. The ORF encodes a protein

25 consisting of 470 amino acid residues and there existed one

96

putative transmembrane domain at the N-terminus. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation

5   product of 61 kDa that was larger than the molecular weight of 52,086 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein CGI-90

10   (Accession No. AAD34085). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein CGI-90 (CG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the

15   present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the entire region.

20   Table 16
_____

HP MSRLGALGGARAGLGLLLGTAAGLGFLCLLYSQRWKRTQRHGRSQSLPNSLDYTQTSDPG

HP RHVMLLRAVPGGAGDASVLPSLPREGQEKVLDRLDFVLTSLVALRREVEELRSSLRGLAG

25

HP EIVGEVRCHMEENQRVARRRRFPFVRERSDSTGSSSVYFTASSGATFTDAESEGGYTTAN

CG   MALAARLWRLLPFRRGAAPGSRLPA

HP AESDNERDSDKESEDGEDEVSCETVKMGRKDSLDLEEEAASGASSALEAGGSSGLEDVLP

                                               .*.   . ..*

CG GPSGSRGIAAPARFRGFEVMGNPGTFNRGLLLSALSYLGFETYQVISQAAVVHATAKVEE

HP LLQQADELHRGDEQGKREGFQLLLNNKLVYGSRQDFLWRLARAYSDMCELT-EEVSEKKS

   .*.*** *. ..* .*   .*** . *   .. ...******* .*. .*. ... .***

CG ILEQADYLYESGETEK--LYQLLTQYK--ESEDAELLWRLARASRDVAQLSRTSEEEKKL

HP YALDGKEEAEAALEKGDESADCHLWYAVLCGQLAEHESIQRRIQSGFSFKEHVDKAIALQ

   . .. * *. ****...* ..* ***. ......*.*. .*.... .*** .***.*.

CG LVYEALEYAKRALEKNESSFASHKWYAICLSDVGDYEGIKAKIANAYIIKEHFEKAIELN

HP PENPMAHFLLGRWCYQVSHLSWLEKKTATALLESPLSATVEDALQSFLKAEELQPGFSKA

   *... . *.* *** ....* ....*. *...* *.* *.** * .**...*.* .

CG PKDATSIHLMGIWCYTFAEMPWYQRRIAKMLFATPPSSTYEKALGYFHRAEQVDPNFYSK

HP GRVYISKCYRELGKNSEARWWMKLALELPDVTKEDLAIQKDLEELEVILRD

   . ....* * .*... * .*.. * . *. *.** .**.. ..* . ...

CG NLLLLGKTYLKLHNKKLAAFWLMKAKDYPAHTEEDKQIQTEAAQLLTSFSEKN

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA852295) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10717> (SEQ ID NOS: 39, 49 and 59)

Determination of the whole base sequence of the cDNA insert of clone HP10717 obtained from cDNA library of human kidney revealed the structure consisting of a 73-bp 5'-untranslated region, a 732-bp ORF, and a 976-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed two putative transmembrane domains. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was larger than the molecular weight of 26,270 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI478174) among ESTs. However, since they are partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present invention.

<HP10718> (SEQ ID NOS: 40, 50 and 60)

Determination of the whole base sequence of the

5   cDNA insert of clone HP10718 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 86-bp 5'-untranslated region, a 813-bp ORF, and a 889-bp 3'-untranslated region. The ORF encodes a protein consisting of 270 amino acid residues and there existed

10   three putative transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was smaller than the molecular weight of

15   31,116 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Caenorhabditis elegans hypothetical protein Y53C10A (Accession No. CAA22139). Table 17 shows the

20   comparison between amino acid sequences of the human protein of the present invention (HP) and Caenorhabditis elegans hypothetical protein Y53C10A (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an

25   amino acid residue similar to that of the protein of the

present invention, respectively. The both proteins shared a
homology of 54.8% in the entire region other than the N-
terminal region.

5   Table 17

```
_____

   HP                                              MAGAEDWPGQ


   CE  MTSSSAASSSTTTSSTMMPDENECLKKEEERFKSPDPAPTLDEEVDIDTLPSMLEDDPNG

10

   HP  QLELDEDEASCCRWGAQHAGARELAALYSPGKRLQEWCSVILCFSLIAHNLVHLLLLARW

       ***.*****..**..** .***** *.. . *.. ... ***. *
   CE  NVVECDLGFKGPRWGPQHAGAKKLASMYSKEKRLQEKVSLFAAIFLFSIVFIN-LLLS-W



15 HP  EDT--PLVILGVVAGALIADFLSGLVHWGADTWGSVELPIVGKAFIRPFREHHIDPTAIT

       *.. *....* * ..*** ******.***.**** . *..*********.******
   CE  ESSIWVSVLVSAVLGIMTADFASGLVHWAADTFGSVE-TWFGRSFIRPFREHHVDPTAIT



   HP  RHDFIETNGDNCLVTLLPLLNMAYKFRTHSPEALEQ--LYPWECFVFCLIIFGTFTNQIH

20     ***..*.*****.. . *** . *. .*. ..*..*  ..* ... * *. ..*****
   CE  RHDIVEVNGDNCMLCVGPLLWILYQQMTYQRDAITQWATFHW--YILLLGIYVALTNQIH



   HP  KWSHTYFGLPRWVTLLQDWHVILPRKHHRIHHVSPHETYFCITTGWLNYPLEKIGFWRRL

       ********* **..**. *.****.**.***.***. *.********.*** *****..
25 CE  KWSHTYFGLPTWVVFLQKAHIILPRSHHKIHHISPHACYYCITTGWLNWPLEYIGFWRKM
```

```
HP  EDLIQGLTGEKPRADDMKWAQKIK

    *  ..  ..**  .**.**.*** *..

CE  EWVVTTVTGMQPREDDLKWATKLQ
```

5   _____

Furthermore, the search of the GenBank using the
base sequences of the present cDNA has revealed the
registration of sequences that shared a homology of 90% or
10   more (for example, Accession No. AA176107) among ESTs.
However, since they are partial sequences, it can not be
judged whether or not they encode the same protein as the
protein of the present invention. In addition, the region
from position 466 to position 778 of the cDNA of the present
15   invention matched with the region from position 2 to
position 314 of human ubiquitin-conjugating enzyme E2
variant 1 (Accession NO. NM_003349) although no match was
observed in another region.

        <HP03745> (SEQ ID NOS: 61, 71 and 81)

20   Determination of the whole base sequence of the
cDNA insert of clone HP03745 obtained from cDNA library of
human kidney revealed the structure consisting of a 99-bp
5'-untranslated region, a 1170-bp ORF, and a 107-bp 3'-
untranslated region. The ORF encodes a protein consisting of
25   389 amino acid residues and there existed at least nine

putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human solute carrier family 7 (Accession No. NP_003974). Table 18 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human solute carrier family 7 (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.0% in the N-terminal region of 397 amino acid residues.

Table 18

_____

HP   MDRGEKIQLKRVFGYWWGTSFLLINIIG

                                .*..***. ..   *.*... *.**

SC MEAREPGRPTPTYHLVPNTSQSQVEEDVSSPPQRSSETMQLKKEISLLNGVSLVVGNMIG

HP AGIFVSPKGVLAYSCMNVGVSLCVWAGCAILAMTSTLCSAEISISFPCSGAQYYFLKRYF

```
   .*********...  . *.** ***  ........** **...... *** * ..   *
SC SGIFVSPKGVLVHT-ASYGMSLIVWAIGGLFSVVGALCYAELGTTITKSGASYAYILEAF


HP GSTVAFLNLWTSLFLGSGVVAG-QALLLAEYSIQPFFPSCSVPKLPKKCLALAMLWIVGI

   *. .**..**.**.. . .. *. .*.* *** ****. * *. . ** * . ....
SC GGFIAFIRLWVSLLVVEPTGQAIIAITFANYIIQPSFPSCDPPYLACRLLAAACICLLTF


HP LTSRGVKEVTWLQIASSVLKVSILSFISLTGVVFLIRGKKENVERFQNAFDAELPDISHL

   ... ** *..*. . ** * *. *.* * .*  . *.**.**... *...*
SC VNCAYVKWGTRVQDTFTYAKVVALIAIIVMGLVKLCQG---HSEHFQDAFEGSSWDMGNL


HP IQAIFQGYFAYSG--------ELKKPRTTIPKCIFTALPLVTVVYLLVNISYLTVLTPR

   *.. . *.***       *.*.* ..* * ...*.**..*.*.*..* ***. .
SC SLALYSALFSYSGWDTLNFVTEEIKNPERNLPLAIGISMPIVTLIYILTNVAYYTVLNIS


HP EILSSDAVAITWADRAFPSLAWIMPFAISTSLFSNLLISIFKSSRPIYLASQEGQLPLLF

   ..*******.*.**..*  ..*..*.*.. * *..* *** *** ....*.**.** *.
SC DVLSSDAVAVTFADQTFGMFSWTIPIAVALSCFGGLNASIFASSRLFFVGSREGHLPDLL


HP NTLNSHS-SPFTAVLLLVTLGSLAIILTSLIDLINYIFFTGSLWSILLMIGILRRRYQEP

   . ... .. .*..*.*. *.. . .*......****. *.  .. * ..* * *..**
SC SMIHIERFTPIPALLFNCTMALIYLIVEDVFQLINYFSFSYWFFVGLSVVGQLYLRWKEP


HP NLSIPYKVKLDF

   . . * *... *
```

SC KRPRPLKLSVFFPIVFCICSVFLVIVPLFTDTINSLIGIGIALSGVPFYFMGVYLPESRR

<HP03747> (SEQ ID NOS: 62, 72 and 82)

5   Determination of the whole base sequence of the cDNA insert of clone HP03747 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 21-bp 5'-untranslated region, a 1047-bp ORF, and a 1324-bp 3'-untranslated region. The ORF encodes a protein
10   consisting of 348 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 22 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro
15   translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,685 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the
20   mature protein starts from proline at position 39.

       The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human endoplasmic reticulum glycoprotein (Accession No. NP_006807). Table 19 shows the
25   comparison between amino acid sequences of the human protein

of the present invention (HP) and human endoplasmic

reticulum glycoprotein (ER). Therein, the marks of -, *,

and . represent a gap, an amino acid residue identical with

that of the protein of the present invention, and an amino

5   acid residue similar to that of the protein of the present

invention, respectively. The both proteins shared a homology

of 54.1% in the entire region.

Table 19

10   _____

HP MAATLGPLGSWQ-QW-RRCLSARD------GSRMLLLLLLLLGSGQGPQQVGAGQTFEYLK

          *.   * ****. ..   *.   *.**** * ......*.. *.**

ER   MAAEGWIWRWGWGRRCLGRPGLLGPGPGPTTPLFLLLL-LGSVTADITDGNS-EHLK

15   HP REHSLSKPYQGVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQ

        ***** *******..* .**.. *..*. .**.***** .**.*..**. ****.***..

     ER REHSLIKPYQGVGSSSMPLWDFQGSTMLTSQYVRLTPDERSKEGSIWNHQPCFLKDWEMH

     HP VHFKIHGQGKKNLHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTYPNEEKQQERVF

20   ****.** *********.*.***.**. ******..*.* **..*.*****.*. ****

     ER VHFKVHGTGKKNLHGDGIALWYTRDRLVPGPVFGSKDNFHGLAIFLDTYPNDET-TERVF

     HP PYISAMVNNGSLSYDHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKH

        ****.**********..*** ***.**** ** ..****..** . .**.* *...*.

25   ER PYISVMVNNGSLSYDHSKDGRWTELAGCTADFRNRDHDTFLAVRYSRGRLTVMTDLEDKN

HP EWRDCIEVPGVRLPRGYYFGTSSITGDLSDNHDVISLKLFELTVERTPEEEKLHRDVFLP

   .....***** *****.*. *********.**.***.* **.**.**..... . *

ER EWKNCIDITGVRLPTGYYFGASAGTGDLSDNHDIISMKLFQLMVEHTPDEESIDWTKIEP

5

HP SVDNMKLP-----EMTAPL--PPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRK

   . .* *   . *. .   **.* ... .*. * *.* ....*.**.. *

ER SVNFLKSPKDNVDDPTGNFRSGPLTGWRVFLLLLCALLGIVVCAVVGAVVFQKRQERN-K

10   HP RFY

         ***

      ER RFY

_____

15   Furthermore, the search of the GenBank using the

base sequences of the present cDNA has revealed the

registration of sequences that shared a homology of 90% or

more (for example, Accession No. AA262924) among ESTs.

However, since they are partial sequences, it can not be

20   judged whether or not they encode the same protein as the

protein of the present invention.

          <HP10719> (SEQ ID NOS: 63, 73 and 83)

          Determination of the whole base sequence of the

cDNA insert of clone HP10719 obtained from cDNA library of

25   human kidney revealed the structure consisting of a 54-bp

5'-untranslated region, a 786-bp ORF, and a 576-bp 3'-untranslated region. The ORF encodes a protein consisting of 261 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative

5   transmembrane domain in the inner portion. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 33 kDa that was larger than the molecular weight of

10   27,435 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from asparagine at position 19.

The search of the protein database using the amino

15   acid sequence of the present protein revealed that the protein was similar to mouse endomucin (Accession No. AAD05208). Table 20 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse endomucin (MM). Therein, the marks of -, *, and .

20   represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 47.9% in the entire region.

25

Table 20

```
HP MELLQVTIL-FLLP-SIC-SSNSTGVL-EAANNSLVVTTTKPSITTPNTESLQKNVVTPT
   * ***.*.* ***. *.* *.....*  ..  ..  ..***.*.*.*.. *. .* .*.
MM MRLLQATVLFFLLSNSLCHSEDGKDVQNDSIPTPAETSTTKASVTIPGIVSV-TNPNKPA
```

```
HP TGTTPKGTITNELLKMSLMSTATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAV
   .**.*.**..... . **..* . **. .... .**.. .*.* . ..**.... .**
MM DGTPPEGTTKSDVSQTSLVTTINSLTTPKHEVGTTTEGPLRNESSTMKITVPNTPTSNAN
```

```
HP STLQSSKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENTSQSQVIGTEGG
   ***..*. *..**           . ... . .*.**           ...... . * . .**.
MM STLPGSQNKITTQ-------LLDALPKITATPS---------ASLTTAHTMSLLQDTEDR
```

```
HP KNASTSATSRSYSSIILPVVIALIVITLSVFVLVGLYRMCWKADPGTPENGNDQPQSDKE
   * *.*..*..************.**** **.******.*** ****************
MM KIATTPSTTPSYSSIILPVVIALVVITLLVFTLVGLYRICWKRDPGTPENGNDQPQSDKE
```

```
HP SVKLLTVKTISHESGEHSAQGKTKN
   *************************
MM SVKLLTVKTISHESGEHSAQGKTKN
```

        The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example,
Accession No. AA486620) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
encode the same protein as the protein of the present
5   invention.

<HP10720> (SEQ ID NOS: 64, 74 and 84)

Determination of the whole base sequence of the
cDNA insert of clone HP10720 obtained from cDNA library of
human kidney revealed the structure consisting of a 25-bp
10   5'-untranslated region, a 669-bp ORF, and a 653-bp 3'-
untranslated region. The ORF encodes a protein consisting of
222 amino acid residues and there existed a putative
secretory signal at the N-terminus and one putative
transmembrane domain in the inner portion. Figure 24 depicts
15   the hydrophobicity/hydrophilicity profile, obtained by the
Kyte-Doolittle method, of the present protein.   In vitro
translation resulted in formation of a translation product
of 28 kDa that was somewhat larger than the molecular weight
of 25,219 predicted from the ORF. In this case, the addition
20   of a microsome led to the formation of a product of 35 kDa.
In addition, there exist in the amino acid sequence of this
protein two sites at which N-glycosylation may occur (Asn-
Val-Thr at position 76 and Asn-His-Thr at position 93).
Application of the (-3,-1) rule, a method for predicting the
25   cleavage site of the secretory signal sequence, allows to

expect that the mature protein starts from glutamic acid at position 15.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of

5   sequences that shared a homology of 90% or more (for example, Accession No. AI792241) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10   <HP10721> (SEQ ID NOS: 65, 75 and 85)

Determination of the whole base sequence of the cDNA insert of clone HP10721 obtained from cDNA library of human kidney revealed the structure consisting of a 74-bp 5'-untranslated region, a 552-bp ORF, and a 1658-bp 3'-

15   untranslated region. The ORF encodes a protein consisting of 183 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the

20   Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was somewhat larger than the molecular weight of 19,989 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 22 kDa.

25   Application of the (-3,-1) rule, a method for predicting the

cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 25.

5   The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R27187) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present

10   invention.

<HP10725> (SEQ ID NOS: 66, 76 and 86)

Determination of the whole base sequence of the cDNA insert of clone HP10725 obtained from cDNA library of human kidney revealed the structure consisting of a 235-bp

15   5'-untranslated region, a 789-bp ORF, and a 713-bp 3'-untranslated region. The ORF encodes a protein consisting of 262 amino acid residues and there existed one putative transmembrane domain. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-

20   Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of

25   sequences that shared a homology of 90% or more (for example,

Accession No. AI127782) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5   <HP10727> (SEQ ID NOS: 67, 77 and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10727 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 102-bp 5'-untranslated region, a 507-bp ORF, and a 947-

10   bp 3'-untranslated region. The ORF encodes a protein consisting of 168 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the

15   Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 24 kDa that was larger than the molecular weight of 17,822 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 23 kDa.

20   Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 29.

The search of the GenBank using the base sequences

25   of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. R80316) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present

5   invention.

<HP10728> (SEQ ID NOS: 68, 78 and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10728 obtained from cDNA library of human umbilical cord blood revealed the structure consisting

10   of a 221-bp 5'-untranslated region, a 732-bp ORF, and a 902-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained

15   by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was larger than the molecular weight of 26,534 predicted from the ORF.

The search of the GenBank using the base sequences

20   of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H23535) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present

25   invention.

<HP10730> (SEQ ID NOS: 69, 79 and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10730 obtained from cDNA library of human umbilical cord blood revealed the structure consisting

5 of a 27-bp 5'-untranslated region, a 1287-bp ORF, and a 1216-bp 3'-untranslated region. The ORF encodes a protein consisting of 428 amino acid residues and there existed one putative transmembrane domain. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-

10 Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was somewhat larger than the molecular weight of 48,992 predicted from the ORF.

The search of the GenBank using the base sequences

15 of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. C19105) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present

20 invention.

<HP10742> (SEQ ID NOS: 70, 80 and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10742 obtained from cDNA library of human umbilical cord blood revealed the structure consisting

25 of a 231-bp 5'-untranslated region, a 852-bp ORF, and a 828-

bp 3'-untranslated region. The ORF encodes a protein

consisting of 283 amino acid residues and there existed two

putative transmembrane domains. Figure 30 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-

5   Doolittle method, of the present protein. In vitro

translation resulted in formation of a translation product

of 30 kDa that was smaller than the molecular weight of

31,629 predicted from the ORF.

Furthermore, the search of the GenBank using the

10   base sequences of the present cDNA has revealed the

registration of sequences that shared a homology of 90% or

more (for example, Accession No. T35949) among ESTs. However,

since they are partial sequences, it can not be judged

whether or not they encode the same protein as the protein

15   of the present invention.

<HP03800> (SEQ ID NOS: 91, 101 and 111)

Determination of the whole base sequence of the

cDNA insert of clone HP03800 obtained from cDNA library of

human umbilical cord blood revealed the structure consisting

20   of a 67-bp 5'-untranslated region, a 1431-bp ORF, and a 135-

bp 3'-untranslated region. The ORF encodes a protein

consisting of 476 amino acid residues and there existed a

putative secretory signal at the N-terminus. Figure 31

depicts the hydrophobicity/hydrophilicity profile, obtained

25   by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 55 kDa that was almost identical with the molecular weight of 54,110 predicted from the ORF. In this case, the addition of a microsome led to the formation of a

5   product of 58 kDa. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Lys-Thr at position 81, Asn-Met-Thr at position 132, Asn-Val-Thr at position 307 and Asn-Gln-Thr at position 346). Application of the (-3,-1)

10   rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 23.

The search of the protein database using the amino acid sequence of the present protein revealed that the

15   protein was similar to mosquito vitellogenic carboxypeptidase (Accession No. P42660). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mosquito vitellogenic carboxypeptidase (VC). Therein, the marks of -, *, and .

20   represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.5% in the entire region. In addition, the C-terminal

25   portion beginning from alanine at position 182 matched with

human probable carboxypeptidase (Accession No. AAC23787) except one amino acid residue.

Table 21

HP   MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPK-GDSGQPLFLTPYIEAGKIQKG

      ...* *. . **. *.**.****** ...***...

VC MVKFHLLVLIAFTCYTCSDATLWNPYKKLMRGSASPPRPGESGEPLFLTPLLQDGKIEEA

HP RELSLVGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSM

   *. . *..   ...**.**.**. ..*******. **. ..*.**...*******.**.

VC RNKARVNHPMLSSVESYSGFMTVDAKHNSNLFFWYVPAKNNREQAPILVWLQGGPGASSL

HP FGLFVEHGPYVVTSNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVAR

   .* *.. . .*.....*...* . *.**************...**..**..*.

VC FGMFEENGPFHIHRNKSVKQREYSWHQNHHMIYIDNPVGTGFSFTDSDEGYSTNEEHVGE

HP DLYSALIQFFQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGD

   .* . . *** .**. .. **..****.**.***... ** *. .. ****.*.****

VC NLMKFIQQFFVLFPNLLKHPFYISGESYGGKFVPAFGYAIH--NSQSQPKINLQGLAIGD

HP GYSDPESIIGGYAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGD

   . . . .*.*.**..**.* . .* *... . *.   ... .* ... *.**

VC GYTDPLNQL-NYGEYLYELGLIDLNGRKKFDEDTAAAIACAERKDMNSANRLIQGLFDG-

```
HP  LTSDPSYFQNVTGCSNYYNFLRC-TEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVE

    *... ***..*** *.****..   .*....   ..*** ****..****. .*.*..   .

VC  LDGQESYFKKVTGFSSYYNFIKGDEESKQDSVLMEFLSNPEVRKGIHVGELPFHDSDGHN
```

5
```
HP  K---YLREDTVQSVKPWLTEIMNNYKVLIYNGQLDIIVAAALTEHSLMGMDWKGSQEYKK

    *    *.***...* **.......*.**.******* * ..* . ** * ..*. ***.

VC  KVAEMLSEDTLDTVAPWVSKLLSHYRVLFYNGQLDIICAYPMTVDFLMKMPFDGDSEYKR
```

```
HP  AEKKVWKIFKSDSEVAGYIRQAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDP
```
10
```
    *...  *.. *.*.*** ..** ...*.**..**..* *** .*****..*

VC  ANRE---IYRVDGEIAGYKKRAGRLQEVLIRNAGHMVPRDQPKWAFDMITSFTHKNYL
```

```
HP  YVG
```

_____

15

The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. AA095665) among ESTs. However, since they are
20 partial sequences, it can not be judged whether or not they
encode the same protein as the protein of the present
invention.

<HP03831> (SEQ ID NOS: 92, 102 and 112)

Determination of the whole base sequence of the
25 cDNA insert of clone HP03831 obtained from cDNA library of

human kidney revealed the structure consisting of a 191-bp
5'-untranslated region, a 681-bp ORF, and a 223-bp 3'-
untranslated region. The ORF encodes a protein consisting of
226 amino acid residues and there existed four putative

5   transmembrane domains. Figure 32 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of high molecular weight.

10   The search of the protein database using the amino
acid sequence of the present protein revealed that the
protein was similar to human claudin-10 (Accession No.
NP_008915). Table 22 shows the comparison between amino
acid sequences of the human protein of the present invention

15   (HP) and human claudin-10 (CD). Therein, the marks of -, *,
and . represent a gap, an amino acid residue identical with
that of the protein of the present invention, and an amino
acid residue similar to that of the protein of the present
invention, respectively. The both proteins shared a homology

20   of 76.2% in the entire region. The C-terminal region
downstream from glycine at position 72 completely matched
with that sequence.

Table 22

25   _____

```
HP   MSRAQIWALVSGVGGFGALVAATTSNEWKVTTRASSVITATWVYQGLWMNCAGNALGS

     ..* *.. ...*.  . .. ... ***.* ...***..  ...**..*.... *

CD   MASTASEIIAFMVSISGWVLVSSTLPTDYWKVSTIDGTVITTATYWANLWKACVTDSTGV
```

```
5    HP   FHCRPHFTIFKVAGYIQACRGLMIAAVSLGFFGSIFALFGMKCTKVGGSDKAKAKIACLA

          .*.   ... ..********************************************

     CD   SNCKDFPSMLALDGYIQACRGLMIAAVSLGFFGSIFALFGMKCTKVGGSDKAKAKIACLA
```

```
     HP   GIVFILSGLCSMTGCSLYANKITTEFFDPLFVEQKYELGAALFIGWAGASLCIIGGVIFC

10        *************************************************************

     CD   GIVFILSGLCSMTGCSLYANKITTEFFDPLFVEQKYELGAALFIGWAGASLCIIGGVIFC
```

```
     HP   FSISDNNKTPRYTYNGATSVMSSRTKYHGGEDFKTTNPSKQFDKNAYV

          ********************************************

15   CD   FSISDNNKTPRYTYNGATSVMSSRTKYHGGEDFKTTNPSKQFDKNAYV
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N41613) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

25   <HP03879> (SEQ ID NOS: 93, 103 and 113)

121

Determination of the whole base sequence of the cDNA insert of clone HP03879 obtained from cDNA library of human kidney revealed the structure consisting of a 33-bp 5'-untranslated region, a 918-bp ORF, and a 651-bp 3'-

5   untranslated region. The ORF encodes a protein consisting of 305 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro

10   translation resulted in formation of a translation product of 34 kDa that was almost identical with the molecular weight of 34,073 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the

15   protein was similar to human NADH-cytochrome b5 reductase (Accession No. Y09501). Table 23 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human NADH-cytochrome b5 reductase (CT). Therein, the marks of -, *, and . represent

20   a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 63.5% in the entire region other than the N-terminal region.

25

Table 23

```
─────────────────────────────────────────────────────────────

   HP  MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHN

                       * .** *..** .*. ** ***.*....**.

5  CT     MGAQLSTLGHMVLFPVWFLYSLLMKLFQRS-TPAITLESPDIKYPLRLIDREIISHD


   HP  TKRFRFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKG

       *.*******...*.******.*****.****.**.*****..**.*.*.********.*.

   CT  TRRFRFALPSPQHILGLPVGQHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKD

10

   HP  VHPKFPEGGKMSQYLDSLKVGDVVEFRGPSGLLTYTGKGHFNIQPNKKSPPEPRVAKKLG

       .*****.********.*...**..*********.* ***.*.*.*.*** * *..*..*

   CT  THPKFPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKKSNPIIRTVKSVG


15 HP  MIAGGTGITPMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW

       **************.****.* *.*.* * ************.** .****......*****

   CT  MIAGGTGITPMLQVIRAIMKDPDDHTVCHLLFANQTEKDILLRPELEELRNKHSARFKLW


   HP  FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQK

20     .***..*..*.*..***...***.***.*... ***.******.* ** ****..*.. .

   CT  YTLDRAPEAWDYGQGFVNEEMIRDHLPPPEEEPLVLMCGPPPMIQYACLPNLDHVGHPTE


   HP  MRFTY

       . *..

25 CT  RCFVF
```

The search of the GenBank using the base sequences

of the present cDNA has revealed the registration of

5   sequences that shared a homology of 90% or more (for example,

Accession No. F06459) among ESTs. However, since they are

partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present

invention.

10   <HP03880> (SEQ ID NOS: 94, 104 and 114)

Determination of the whole base sequence of the

cDNA insert of clone HP03880 obtained from cDNA library of

human kidney revealed the structure consisting of a 98-bp

5'-untranslated region, a 684-bp ORF, and a 115-bp 3'-

15   untranslated region. The ORF encodes a protein consisting of

227 amino acid residues and there existed a putative

secretory signal at the N-terminus. Figure 34 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein.   In vitro

20   translation resulted in formation of a translation product

of 28 kDa that was somewhat larger than the molecular weight

of 25,717 predicted from the ORF. In this case, the addition

of a microsome led to the formation of a product of 27 kDa.

Application of the (-3,-1) rule, a method for predicting the

25   cleavage site of the secretory signal sequence, allows to

expect that the mature protein starts from aspartic acid at position 23.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rat phosphatidylethanolamine-binding protein (Accession No. P31044). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat phosphatidylethanolamine-binding protein (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.6% in the region of 133 amino acid residues other than the N-terminal region.

Table 24

HP MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV

RN   MAADISQWAGPLSLQEVDEPPQHALRVDYGGVTV

HP VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG

    ... *   * *.**..******* .*. * *.*.**...**

RN DELGKVLTPTQVMNRPSSISWDGLDPGKLYTLVLTDPDAPSRKDPKFREWHHFLVVNMKG

HP ADLKKGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKV---ISLLP-KENKTRGSWK

   .*...*..   **.* ...** ..*.*** ..** ** .   ..*. *....**..*

RN NDISSGTV----LSEYVGSGPPKDTGLHRYVWLVYEQEQPLNCDEPILSNKSGDNRGKFK

HP MDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNQAEIAAC

   ...* ...***.* *.* * .. .. *.*.

RN VESFRKKYHLGAPVAGTCFQAEWDDSVPKLHDQLAGK

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H83784) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10704> (SEQ ID NOS: 95, 105 and 115)

Determination of the whole base sequence of the cDNA insert of clone HP10704 obtained from cDNA library of human kidney revealed the structure consisting of a 141-bp 5'-untranslated region, a 1326-bp ORF, and a 399-bp 3'-untranslated region. The ORF encodes a protein consisting of 441 amino acid residues and there existed eight putative transmembrane domains.   Figure   35   depicts   the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5   The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human unknown gene product (Accession No. AAC27544). Table 25 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human unknown gene product (UP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 39.1% in the entire region.

Table 25

HP   MAIHKALVMCLGLPLFLFPG-AWAQGHVPPGCSQGLNPLYYNLCDRSGAWGIVLE

20   * **.... * ... ...**. .* * * .*** .. ****.*

UN MFVASERKMRAHQVLTFLLLFVITSVASENASTSRGCGLDLLPQYVSLCDLDAIWGIVVE

HP AVAGAGIVTTFVLTIILVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVVKPDFS

   ****** ..*..* .**...***.....*.* .* . .********* *.** ... * .

25 UN AVAGAGALITLLLMLILLVRLPFIKEKEKKSPVGLHFLFLLGTLGLFGLTFAFIIQEDET

```
HP  TCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVIFTVALLLTLVEVIINTEW
    .*. ****.*****.*****  .... .. *.*.. ** ** . ..** * **.***..**
UN  ICSVRRFLWGVLFALCFSCLLSQAWRVRRLVRHGTGPAGWQLVGLALCLMLVQVIIAVEW
```

5

```
HP  LIITLVRGSGEGGPQGNSSAGWAVASPCAIANMDFVMALIYVMLLLLGAFLGAWPALCGR
    *..*..*           ..      ..** . ********* *.**. ..  *  .***.
UN  LVLTVLR-------DT--------RPACAYEPMDFVMALIYDMVLLVVTLGLALFTLCGK
```

10

```
HP  YKRWRKHGVFVLLTTATSVAIWVVWIVMYTYGN-KQHNSPTWDDPTLAIALAANAWAFVL
    .***. .*.*.*.*.   ** ***.*..** .** * ... .*.******.***..*.**.
UN  FKRWKLNGAFLLITAFLSVLIWVAWMTMYLFGNVKLQQGDAWNDPTLAITLAASGWVFVI
```

```
HP  FYVIPEVSQVTKSSPEQSYQGDMYPTRGVGY-ETILKEQ-KGQSMFVENKAFSMDEPVAA
```

15

```
    *..***. . * .. *.   . . *.      ** ..*. . .. ..*********. **
UN  FHAIPEI-HCTLLPALQENTPNYFDTSQPRMRETAFEEDVQLPRAYMENKAFSMDEHNAA
```

```
HP  KRPVS-PYSGYNGQLLTSVYQPTEMALMHKVPSEGAYDIILPRATANSQVMGSANSTLRA
    *... *  .. . .*. .... ... .*   .. ...* .* .. . ... *.
```

20

```
UN  LRTAGFPNGSLGKRPSGSLGKRPSAPFRSNVYQPTEMAVVLNGGTIPTAPPSHTGRHLW
```

```
HP  EDMYSAQSHQAATPPKDGKNSQVFRNPYVWD
```

---

25   The search of the GenBank using the base sequences

128

of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. AA346702) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they

5   encode the same protein as the protein of the present
invention.

<HP10715> (SEQ ID NOS: 96, 106 and 116)

Determination of the whole base sequence of the
cDNA insert of clone HP10715 obtained from cDNA library of

10   human umbilical cord blood revealed the structure consisting
of a 49-bp 5'-untranslated region, a 798-bp ORF, and a 1351-
bp 3'-untranslated region. The ORF encodes a protein
consisting of 265 amino acid residues and there existed two
putative transmembrane domains. Figure 36 depicts the

15   hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 43 kDa that was larger than the molecular weight of
29,217 predicted from the ORF.

20   The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. AI381750) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they

25   encode the same protein as the protein of the present

invention.

<HP10724> (SEQ ID NOS: 97, 107 and 117)

Determination of the whole base sequence of the
cDNA insert of clone HP10724 obtained from cDNA library of
5   human umbilical cord blood revealed the structure consisting
of a 68-bp 5'-untranslated region, a 627-bp ORF, and a 1485-
bp 3'-untranslated region. The ORF encodes a protein
consisting of 208 amino acid residues and there existed one
putative transmembrane domain at the N-terminus. Figure 37
10   depicts the hydrophobicity/hydrophilicity profile, obtained
by the Kyte-Doolittle method, of the present protein. In
vitro translation resulted in formation of a translation
product of 24 kDa that was almost identical with the
molecular weight of 23,850 predicted from the ORF.

15   The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. T78035) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
20   encode the same protein as the protein of the present
invention.

<HP10733> (SEQ ID NOS: 98, 108 and 118)

Determination of the whole base sequence of the
cDNA insert of clone HP10733 obtained from cDNA library of
25   human umbilical cord blood revealed the structure consisting

of a 102-bp 5'-untranslated region, a 1203-bp ORF, and a 222-bp 3'-untranslated region. The ORF encodes a protein consisting of 400 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was larger than the molecular weight of 43,151 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Leu-Thr at position 52, Asn-Ala-Ser at position 131, Asn-Ile-Thr at position 145 and Asn-Leu-Ser at position 343). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from arginine at position 33.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Drosophila melanogaster GOLIATH protein (Accession No. Q06003). Table 26 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Drosophila melanogaster

GOLIATH protein (DM). Therein, the marks of -, *, and .

represent a gap, an amino acid residue identical with that

of the protein of the present invention, and an amino acid

residue similar to that of the protein of the present

5   invention, respectively. The both proteins shared a homology

of 35.0% in the entire region.

Table 26

_____

10   HP MAWRRREASVGARGVLALALLALALCVPGARGRALEWFSAVVNIEYVDPQTNLTVWSVSE

     HP SGRFGDSSPKEGAHGLVGVPWAPGGDLEGCAPDTRFFVPEPGGRGAAPWVALVARGGCTF

     HP KDKVLVAARRNASAVVLYNEERYGNITLPMSHAGTGNIVVIMISYPKGREILEL-VQKGI
                              *   *... .. .*.*.. . .*.* ..**
15   DM   MQLEKMQIKGKTRNIAAVITYQNIGQDLSLTLDKGY

     HP PVTMTIGVGTRHVQEF--ISGQSVVFVAIAFITMMIISLAWLIFYYIQRFLY-TGSQIGS
        ..* * * *... .. **..*.** . * ********* * ... *
20   DM NVTISIIEGRRGVRTISSLNRTSVLFVSISFI--VDDILCWLIFYYIQRFRYMQAKDQQS

     HP QSHRKETKKVIGQLLLHTVKHGEKGIDVDAENCAVCIENFKVKDIIRILPCKHIFHRICI
        .. . ***.* .. .* * ... *.*.. **.***..* .*.******* **. **
     DM RNLCSVTKKAIMKIPTKTGKFSD-EKDLDSDCCAICIEAYKPTDTIRILPCKHEFHKNCI

25

HP DPWLLDHRTCPMCKLDVIKALGYWGEPGDVQEMPAPESPPGRDPAANLSLALPDDDGSDE

    ****..***********.* **   ... . *.*. .. ..

DM DPWLIEHRTCPMCKLDVLKFYGY-VVGDQIYQTPSPQHTAPIASIEEVPVIVVAVPHGPQ

5   HP SSPPSASPAESEPQCDPSFKGDAGENTALLEAGRSDSRHGGPIS

    . .* .... *. . .. *... . ....

DM PLQPLQASNMSSFAPSHYFQSSRSPSSSVQQQLAPLTYQPHPQQAASERGRRNSAPATMP

---

10   The search of the GenBank using the base sequences

of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example,

Accession No. AI286184) among ESTs. However, since they are

partial sequences, it can not be judged whether or not they

15   encode the same protein as the protein of the present

invention.

    <HP10734> (SEQ ID NOS: 99, 109 and 119)

    Determination of the whole base sequence of the

cDNA insert of clone HP10734 obtained from cDNA library of

20   human umbilical cord blood revealed the structure consisting

of a 124-bp 5'-untranslated region, a 579-bp ORF, and a

1202-bp 3'-untranslated region. The ORF encodes a protein

consisting of 192 amino acid residues and there existed one

putative transmembrane domain. Figure 39 depicts the

25   hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino

5   acid sequence of the present protein revealed that the protein was similar to human sodium channel ß2 subunit (Accession No. AAD47196). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human sodium channel ß2 subunit

10   (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 26.3% in the N-terminal

15   region of 152 amino acid residues.

Table 27

HP   MFCPLKLILLPVLLDYSLGLNDLNVS-PPELTVHVGDSALMGCVFQS--TEDK

20   ...*. *.....   ....*. *..*.* *..* . *.*.* * ..

SC MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNH

HP CIFKIDWTLSPGEHAKDE-YVLYYYSNLSVPIGRFQNRVHLMGDNLCNDGSLLLQDVQEA

        *...**   .. ..* .. .   .   ..***.**.. *.   * *..*..** .

25   SC KQFSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMLRNVQPE

HP DQGTYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVE

   ..* * *.   ...   . . *.** *** *   *. ..

SC DEGIYNCYIMNPPDRHRGHGKIHLQVLMEEPPERDFTVAVIVGASVGGFLAVVILVLMVV

HP WIFSGRRAKVTRRKHHCVREGSG

SC KCVRRKKEQKLSTDDLKTEEEGKTDGEGNPDDGAK

_____

        The search of the GenBank using the base sequences

of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example,

Accession No. C03216) among ESTs. However, since they are

partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present

invention.

        <HP10756> (SEQ ID NOS: 100, 110 and 120)

        Determination of the whole base sequence of the

cDNA insert of clone HP10756 obtained from cDNA library of

human kidney revealed the structure consisting of a 49-bp

5'-untranslated region, a 783-bp ORF, and a 166-bp 3'-

untranslated region. The ORF encodes a protein consisting of

260 amino acid residues and there existed a putative

secretory signal at the N-terminus. Figure 40 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 27,356 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW027769) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03670> (SEQ ID NOS: 121, 131 and 141)

Determination of the whole base sequence of the cDNA insert of clone HP03670 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 77-bp 5'-untranslated region, a 1014-bp ORF, and a 531-bp 3'-untranslated region. The ORF encodes a protein consisting of 337 amino acid residues and there existed at least seven putative transmembrane domains. Figure 41 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein KIAA0260

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(Accession No. BAA13390).　Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein KIAA0260　(KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 57.6% in the entire region other than the N-terminal region.　In addition, the C-terminal region beginning from leucine at position 77 matched with human putative Sqv-7-like protein (Accession No. AJ005866) except one amino acid residue.

Table 28

```
_____

HP                                        MTAGGQAEAEGAGGEPG


KI NSWSPLGAAAAGPRAARPRRQATAAAAAMAEVHRRQHARVKGEAPAKSSTLRDEEELGMA


HP AARLPSRVARLLSALFYGTCSFLIVLVNKALLTTYGFPSPIFLGIGQMAATIMILYVSKL
   .**.* ***..*****.***..**.* ***.. .*.***.**. .*.*.*
KI SAETLTVFLKLLAAGFYGVSSFLIVVVNKSVLTNYRFPSSLCVGLGQMVATVAVLWVGKA


HP NKIIHFPDFDKKIPVKLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLETI
   ....***.*...* * ******* **.*.** **.**.*******.*.* .*.. *..
```

KI LRVVKFPDLDRNVPRKTFPLPLLYFGNQITGLFSTKKLNLPMFTVLRRFSILFTMFAEGV

HP ILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLNDIFTAANGVYTKQKMDPK

   .* * .* .* ..***.*.***.**.*****.**** *...**..*****.*.***.*.*

KI LLKKTFSWGIKMTVFAMIIGAFVAASSDLAFDLEGYAFILINDVLTAANGAYVKQKLDSK

HP ELGKYGVLFYNACFMIIPTLIISVSTGDLQQATEFNQWKNVVFILQFLLSCFLGFLLMYS

   ******.*.*** ***.*** *.   *** *.*.**. * ...*.*** *** .**.***.

KI ELGKYGLLYYNALFMILPTLAIAYFTGDAQKAVEFEGWADTLFLLQFTLSCVMGFILMYA

HP TVLCSYYNSALTTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRYSFLTL

   ****. *******..** ***. ..***...******. **.****..**.* **..*.

KI TVLCTQYNSALTTTIVGCIKNILITYIGMVFGGDYIFTWTNFIGLNISIAGSLVYSYITF

HP SSQLKPKPVGEENICLDLKS

   ... .*. .*.* **.*.

KI TEEQLSKQ-SEANNKLDIKGKGAV

        The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. R24922) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
encode the same protein as the protein of the present

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invention.

<HP03688> (SEQ ID NOS: 122, 132 and 142)

Determination of the whole base sequence of the cDNA insert of clone HP03688 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 35-bp 5'-untranslated region, a 711-bp ORF, and a 1729-bp 3'-untranslated region. The ORF encodes a protein consisting of 236 amino acid residues and there existed five putative transmembrane domains. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Caenorhabditis elegans hypothetical protein W02D9 (Accession No. CAB03470). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Caenorhabditis elegans hypothetical protein W02D9 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 50.8% in the entire region other than the N-terminal

region.

Table 29

---

5   HP   MAEAEE

       CE MEILNLSSKFSLSDKPCQKFIFSLFSAVQNSRFKIISFPEIHQKPLPQEEMNSFGNASVD

       HP SPGDPGTASPRPLFAGLSDISISQDIPVEGEITIPMRSRIREFDSSTLNESVRNTIMRDL

10   **..   . . .**.*.*..*..**.

       CE IDMLEQEMAAEQTANLSGNIAGMSAPKSSSNRRGPMQEVDLDAEFDTLEEPVWDTVKRDV

       HP KAVGKKFMHVLYPR-KSNTLLRDWDLWGPLILCVTLALMLQRDSADSEKDGGPQFAEVFV

          .** ** **. *. ... **********..**.***.**.   .......***..**.

15   CE LTVGAKFTHVVLPHGDKQQLLRDWDLWGPLFICVGLALLLQH---NGGTESAPQFTQVFT

       HP IVWFGAVTITLNSKLLGGNISFFQSLCVLGYCILPLTVAMLICRLVLLADPGPVNFMVRL

          *..**.*..* * **************.***.** ** ..*.* .* .   .* .**

       CE ITFFGSVIVTANIKLLGGNISFFQSLCVIGYCLLPPFVAAVLCSL-FLHGI---AFPLRL

20

       HP FVVIVMFAWSIVASTAFLADSQPPNRRALAVYPVFLFYFVISWMILTFTPQ

          ... . *.**. ** .***..** ..* *..*********.****..

       CE LITSIGFVWSTYASMGFLAGCQPDKKRLLVIYPVFLFYFVVSWMIISHS

25

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T51465) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03825> (SEQ ID NOS: 123, 133 and 143)

Determination of the whole base sequence of the cDNA insert of clone HP03825 obtained from cDNA library of human kidney revealed the structure consisting of a 20-bp 5'-untranslated region, a 1683-bp ORF, and a 36-bp 3'-untranslated region. The ORF encodes a protein consisting of 560 amino acid residues and there existed seven putative transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 56 kDa that was smaller than the molecular weight of 64,047 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Mycobacterium tuberculosis hypothetical protein Rv0235c (Accession No. CAB07001). Table 30 shows the comparison between amino acid sequences

of the human protein of the present invention (HP) and

Mycobacterium tuberculosis hypothetical protein Rv0235c (MT).

Therein, the marks of -, *, and . represent a gap, an amino

acid residue identical with that of the protein of the

5   present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The

both proteins shared a homology of 41.7% in the entire

region other than the N-terminal region. In addition, the

region from alanine at position 293 to proline at position

10   502 matched with human putative novel protein c360B4.1

(Accession No. CAB56180).

Table 30

---

15   HP MAAPAESLRRRKTGYSDPEPESPPAPGRGPAGSPAHLHTGTFWLTRIVLLKALAFVYFVA

                              . . ..**.*..* .. *..*..*

     MT   MGWFSAPEYWLGRLALERGTAIIYLIA

HP FLVAFHQNKQLIGDRGLLPCRVFLKNFQQYFQDRTSWEVFSYMPTILWLMDWSDMNSNLD

20   *..*.* ..***..*.** . .* . * .... *.*   .. . * ... *.

MT FVAAAQQFRPLIGEHGMLPVPRYLAG-QSFWRTPSIFH-FRYSDRVFAGVCW--LGAVLS

HP LLALLGLGISSFVLITGCANMLLMAALWGLYMSLVNVGHVWYSFGWESQLLETGFLGIFL

     * . * .*** . *.**. .** **.*.****..******* ******* ***

25   MT --AAVVAGAASFVPLW--ATMLIWLTLWVLYLSIVNVGQAWYSFGWESLLLETGFLMIFL

HP CPLWTLSRLPQHTPTSRIVLWGFRWLIFRIMLGAGLIKIRGDRCWRDLTCMDFHYETQPM

　　.*　　　　　.*.　..*.　***.**.　.******.***.***.***.　.*.*****

MT GNERT-------APPILTLLLA-RWLLFRVEFGAGLIKMRGDSCWRSLTCLYYHHETQPM

HP PNPVAYYLHHSPWWFHRFETLSNHFIELLVPFFLFLGRRACIIHGVLQILFQAVLIVSGN

　　......**　*　.**.*.　.***　.*.***　**　..*　*　...　..　*　*..***

MT PGPLSWFFHHLPKPLHRIEVAGNHFAQLVVPFGLFTPQPAASIAAAIIVVTQLWLVASGN

HP LSFLNWLTMVPSLACFDDATLGFLFPSGPGSLKDRVLQMQRDIRGARPEPRFGSVVRRAA

　　.*.*****..　***　　....　　.*...*　　*.*.　.　.　*　..*...*　　.

MT FSWLNWLTIL--LAC---SAID--TSS-AAAL----LPMPAQPALSAPPQWFAGLV---V

HP NVSLGVLLAWLSVPVVLNLLSSRQVMNTHFNSLHIVNTYGAFGSITKERAEVILQGTASS

　　.　.***　**　　.　*****.*　**　　**..*.**********　..*　**...**..*

MT VFTAAVLL--LSYWPARNLLSSHQRMNMSFNPFHLVNTYGAFGSICRTRREVVIEGTDES

HP NASAPDAMWEDYEFKCKPGDPSRRPCLISPYHYRLDWLMWFAAFQTYEHNDWIIHLAGKL

　　.　.　...*..****　*****.*　*　.***　**********.　.　　　*....　..*

MT -PITEQTVWKAYEFKGKPGDPRRLPRQWAPYHLRLDWLMWFAAISPGYALPWMTPFLNRL

HP LASDAEALSLLAHNPFAGRPPPRWVRGEHYRYKFSRPGGRHAAEGKWWVRKRIGAYFPPL

　　*　.*...*.**　****.　..***.**..　*.*.*.　..　.　.　**　*.　**　*　**.

MT LRNDPATLKLLRHNPFP-QSPPRYVRAQLYQYRFTTVAELRRDRA-WWHRTLIGRYVPPM

HP SLEELRPYFRDRGWPLPGPL

   ** ..

MT SLRKVASPPAD

_____

5

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA019047) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03877> (SEQ ID NOS: 124, 134 and 144)

Determination of the whole base sequence of the cDNA insert of clone HP03877 obtained from cDNA library of human kidney revealed the structure consisting of a 106-bp 5'-untranslated region, a 1221-bp ORF, and a 678-bp 3'-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed four putative transmembrane domains. Figure 44 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 49 kDa that was somewhat larger than the molecular weight of 46,208 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Caenorhabditis elegans hypothetical protein Y37D8A (Accession No. CAA21543). Table 31 shows the

5   comparison between amino acid sequences of the human protein of the present invention (HP) and Caenorhabditis elegans hypothetical protein Y37D8A (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino

10   acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 50.2% in the intermediate region of 329 amino acid residues.

15   Table 31

HP   MAENG

CE MAKKQKKSTEKSERTVEFKEPPKPANSEERLVSTRQFLAKIGQKKLIKKKVKNFRFSKKT

20

HP KNCDQRRVAMNKEHHNGNFTDPSSVNEKKRREREERQNIVLWRQPLITLQYFSLEILVIL
                          .* **..**.**.* *...* .** .
CE FIDFFSENQKKNCRLKPAGRGMKPSPSQNTLNRMERETIVFWRRPHIVIPYALMEIAHLA

25   HP KEWTSKLWHRQSIVVSFLLLLAVLIATYYVEGVHQQYVQRIEKQFLLYAYWIGLGILSSV

```
       *    *.  ......    . ... . .*.. *.**..** ***..* ...*. **.***.
CE VELFFKILAHKTVLLLTAISIGLAVYGYHAPGAHQEHVQTIEKHILWWSWWVLLGVLSSI


HP GLGTGLHTFLLYLGPHIASVTLAAYECNSVNFPEPPYPDQIICPDEEGTEGTISLWSIIS

      ***.******.*******.**.*****.*..**.****. * **.....  ....* *..
CE GLGSGLHTFLIYLGPHIAAVTMAAYECQSLDFPQPPYPESIQCPSTKSSI-AVTFWQIVA


HP KVRIEACMWGIGTAIGELPPYFMARAARLSGAEPDDEEYQEFEEML---EHAESAQDFA-

      ***.*. .** ***.*************.**.*******.** *..    ......*...
CE KVRVESLLWGAGTALGELPPYFMARAARISGQEPDDEEYREFLELMNADKESDADQKLSI


HP -SRAKLAVQKLVQKVGFFGILACASIPNPLFDLAGITCGHFLVPFWTFFGATLIGKAIIK

      .*** *.. ....** *** ***********************.**********..*
CE VERAKSWVEHNIHRLGFPGILLFASIPNPLFDLAGITCGHFLVPFWSFFGATLIGKALVK


HP MHIQKIFVIITFSKHIVEQMVAFIGAVPGIGPSLQKPFQEYLEAQRQKLHHKSEMGTPQG

      **.*. ***..**.* .*..* ... .*..** ...*. . ** **. **...  . *.
CE MHVQMGFVILAFSDHHAENFVKILEKIPAVGPYIRQPISDLLEKQRKALHKTPGEHSEQD


HP ENWLSWMFEKLVVVMVCYFILSIINSMAQSYAKRIQQRLNSEEKTK


CE LIDEENQSFEEEEEEAVTPPSSCPLLLSDGFEGVVVKK
```

The search of the GenBank using the base sequences

of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T18977) among ESTs. However, since they are partial sequences, it can not be judged whether or not they

5 encode the same protein as the protein of the present invention.

<HP10765> (SEQ ID NOS: 125, 135 and 145)

Determination of the whole base sequence of the cDNA insert of clone HP10765 obtained from cDNA library of

10 human umbilical cord blood revealed the structure consisting of a 30-bp 5'-untranslated region, a 1362-bp ORF, and a 166-bp 3'-untranslated region. The ORF encodes a protein consisting of 453 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative

15 transmembrane domain in the inner portion. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 48 kDa that was almost identical with the molecular

20 weight of 47,724 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792834) among ESTs. However, since they are

25 partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present invention.

<HP10766> (SEQ ID NOS: 126, 136 and 146)

Determination of the whole base sequence of the

5   cDNA insert of clone HP10766 obtained from cDNA library of human kidney revealed the structure consisting of a 150-bp 5'-untranslated region, a 180-bp ORF, and a 675-bp 3'-untranslated region. The ORF encodes a protein consisting of 59 amino acid residues and there existed two putative

10   transmembrane domains. Figure 46 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa or less that was almost identical with the

15   molecular weight of 6,098 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T85491) among ESTs. However, since they are

20   partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10770> (SEQ ID NOS: 127, 137 and 147)

Determination of the whole base sequence of the

25   cDNA insert of clone HP10770 obtained from cDNA library of

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human kidney revealed the structure consisting of a 150-bp 5'-untranslated region, a 633-bp ORF, and a 186-bp 3'-untranslated region. The ORF encodes a protein consisting of 210 amino acid residues and there existed two putative transmembrane domains. Figure 47 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was larger than the molecular weight of 22,156 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792771) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10772> (SEQ ID NOS: 128, 138 and 148)

Determination of the whole base sequence of the cDNA insert of clone HP10772 obtained from cDNA library of human kidney revealed the structure consisting of a 19-bp 5'-untranslated region, a 498-bp ORF, and a 724-bp 3'-untranslated region. The ORF encodes a protein consisting of 165 amino acid residues and there existed four putative transmembrane domains. Figure 48 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5   The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. F11871) among ESTs. However, since they are partial sequences, it can not be judged whether or not they

10   encode the same protein as the protein of the present invention.

<HP10773> (SEQ ID NOS: 129, 139 and 149)

Determination of the whole base sequence of the cDNA insert of clone HP10773 obtained from cDNA library of

15   human kidney revealed the structure consisting of a 186-bp 5'-untranslated region, a 489-bp ORF, and a 499-bp 3'-untranslated region. The ORF encodes a protein consisting of 162 amino acid residues and there existed four putative transmembrane domains. Figure 49 depicts the

20   hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the GenBank using the base sequences

25   of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. N33828) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10776> (SEQ ID NOS: 130, 140 and 150)

Determination of the whole base sequence of the cDNA insert of clone HP10776 obtained from cDNA library of human kidney revealed the structure consisting of a 207-bp 5'-untranslated region, a 666-bp ORF, and a 139-bp 3'-untranslated region. The ORF encodes a protein consisting of 221 amino acid residues and there existed three putative transmembrane domains. Figure 50 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was larger than the molecular weight of 24,883 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI929639) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs and eukaryotic cells expressing these DNAs. Since all of the proteins of the present invention are secreted or exist in the cell membrane, they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for expressing these proteins in large quantities. Cells into which these genes are introduced to express these proteins can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibody of the present invention can be utilized for the detection, quantification, purification and the like of the protein of the present invention.

The present invention also provides genes

corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include

5   contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements.

10 The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate

15 genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified

20 expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and

25 Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254;

Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and

Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39;

all of which are incorporated by reference herein).

Transgenic animals that have multiple copies of the gene(s)

5   corresponding to the polynucleotide sequences disclosed

herein, preferably produced by transformation of cells with

genetic constructs that are stably maintained within the

transformed cells and their progeny, are provided.

Transgenic animals that have modified genetic control

10 regions that increase or reduce gene expression levels, or

that change temporal or spatial patterns of gene expression,

are also provided (see European Patent No. 0 649 464 B1,

incorporated by reference herein). In addition, organisms

are provided in which the gene(s) corresponding to the

15 polynucleotide sequences disclosed herein have been

partially or completely inactivated, through insertion of

extraneous sequences into the corresponding gene(s) or

through deletion of all or part of the corresponding gene(s).

Partial or complete gene inactivation can be accomplished

20 through insertion, preferably followed by imprecise excision,

of transposable elements (Plasterk, 1992, Bioessays 14(9):

629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA

90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci.

USA 91(2): 719-722; all of which are incorporated by

25 reference herein), or through homologous recombination,

preferably detected by positive/negative genetic selection
strategies (Mansour et al., 1988, Nature 336: 348-352; U.S.
Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153;
5,614, 396; 5,616,491; and 5,679,523; all of which are

5   incorporated by reference herein). These organisms with
altered gene expression are preferably eukaryotes and more
preferably are mammals. Such organisms are useful for the
development of non-human models for the study of disorders
involving the corresponding gene(s), and for the development

10   of assay systems for the identification of molecules that
interact with the protein product(s) of the corresponding
gene(s). Where the protein of the present invention is
membrane-bound (e.g., is a receptor), the present invention
also provides for soluble forms of such protein. In such

15   forms part or all of the intracellular and transmembrane
domains of the protein are deleted such that the protein is
fully secreted from the cell in which it is expressed. The
intracellular and transmembrane domains of proteins of the
invention can be identified in accordance with known

20   techniques for determination of such domains from sequence
information.

Proteins and protein fragments of the present
invention include proteins with amino acid sequence lengths
that are at least 25% (more preferably at least 50%, and

25   most preferably at least 75%) of the length of a disclosed

protein and have at least 60% sequence identity (more

preferably, at least 75% identity; most preferably at least

90% or 95% identity) with that disclosed protein, where

sequence identity is determined by comparing the amino acid

5   sequences of the proteins when aligned so as to maximize

overlap and identity while minimizing sequence gaps. Also

included in the present invention are proteins and protein

fragments that contain a segment preferably comprising 8 or

more (more preferably 20 or more, most preferably 30 or

10   more) contiguous amino acids that shares at least 75%

sequence identity (more preferably, at least 85% identity;

most preferably at least 95% identity) with any such segment

of any of the disclosed proteins.

            Species homologs of the disclosed polynucleotides

15   and proteins are also provided by the present invention. As

used herein, a "species homologue" is a protein or

polynucleotide with a different species of origin from that

of a given protein or polynucleotide, but with significant

sequence similarity to the given protein or polynucleotide,

20   as determined by those of skill in the art. Species homologs

may be isolated and identified by making suitable probes or

primers from the sequences provided herein and screening a

suitable nucleic acid source from the desired species.

            The invention also encompasses allelic variants of

25   the disclosed polynucleotides or proteins; that is,

naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 32

Stringency Condition	Poly-nucleotide Hybrid	Hybrid Length (bp)[†]	Hybridization Temperature and Buffer[†]	Wash Temperature and Buffer[†]
A	DNA : DNA	≥50	65°C; 1×SSC −or− 42°C; 1×SSC,50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T_B*; 1×SSC	T_B*; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC −or− 45°C; 1×SSC,50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T_D*; 1×SSC	T_D*; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC −or− 50°C; 1×SSC,50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T_F*; 1×SSC	T_F*; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC −or− 42°C; 4×SSC,50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T_H*; 4×SSC	T_H*; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC −or− 45°C; 4×SSC,50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T_J*; 4×SSC	T_J*; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC −or− 50°C; 4×SSC,50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T_L*; 2×SSC	T_L*; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC −or− 40°C; 6×SSC,50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T_N*; 6×SSC	T_N*; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC −or− 42°C; 6×SSC,50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T_P*; 6×SSC	T_P*; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC −or− 45°C; 6×SSC,50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T_R*; 4×SSC	T_R*; 4×SSC

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‡ : The hybrid length is that anticipated for the
hybridized region(s) of the hybridizing polynucleotides.
When hybridizing a polynucleotide to a target polynucleotide
of unknown sequence, the hybrid length is assumed to be that
5   of the hybridizing polynucleotide. When polynucleotides of
known sequence are hybridized, the hybrid length can be
determined by aligning the sequences of the polynucleotides
and identifying the region or regions of optimal sequence
complementarity.

10   † : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH_2PO_4, and 1.25mM
EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl
and 15mM sodium citrate) in the hybridization and wash
buffers; washes are performed for 15 minutes after
hybridization is complete.

15      $*T_B - T_R$: The hybridization temperature for hybrids
anticipated to be less than 50 base pairs in length should
be 5-10°C less than the melting temperature (T_m) of the
hybrid, where T_m is determined according to the following
equations. For hybrids less than 18 base pairs in length,
20   T_m(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids
between 18 and 49 base pairs in length, T_m(°C)=81.5 +
16.6(log_{10}[Na^+]) + 0.41 (%G+C) - (600/N), where N is the
number of bases in the hybrid, and [Na^+] is the concentration
of sodium ions in the hybridization buffer ([Na^+] for
25   1×SSC=0.165M).

Additional examples of stringency conditions for

polynucleotide hybridization are provided in Sambrook, J.,

E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A

5   Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold

Spring Harbor, NY, chapters 9 and 11, and Current Protocols

in Molecular Biology, 1995, F.M. Ausubel et al., eds., John

Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated

herein by reference.

10   Preferably, each such hybridizing polynucleotide

has a length that is at least 25% (more preferably at least

50%, and most preferably at least 75%) of the length of the

polynucleotide of the present invention to which it

hybridizes, and has at least 60% sequence identity (more

15   preferably, at least 75% identity; most preferably at least

90% or 95% identity) with the polynucleotide of the present

invention to which it hybridizes, where sequence identity is

determined by comparing the sequences of the hybridizing

polynucleotides when aligned so as to maximize overlap and

20   identity while minimizing sequence gaps.

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CLAIMS

1.   A protein comprising any one of an amino acid sequence selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

2.   An isolated DNA encoding the protein according to Claim 1.

3.   An isolated cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140.

4.   The cDNA according to Claim 3 consisting of any one of a base sequence selected from the group consisting of SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150.

5.   An expression vector that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 by in vitro translation or in eukaryotic cells.

6.   A transformed eukaryotic cell that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 and of producing the protein according to Claim 1.

7.   An antibody directed to the protein according to Claim 1.

Fig.1

Fig.2

3/50
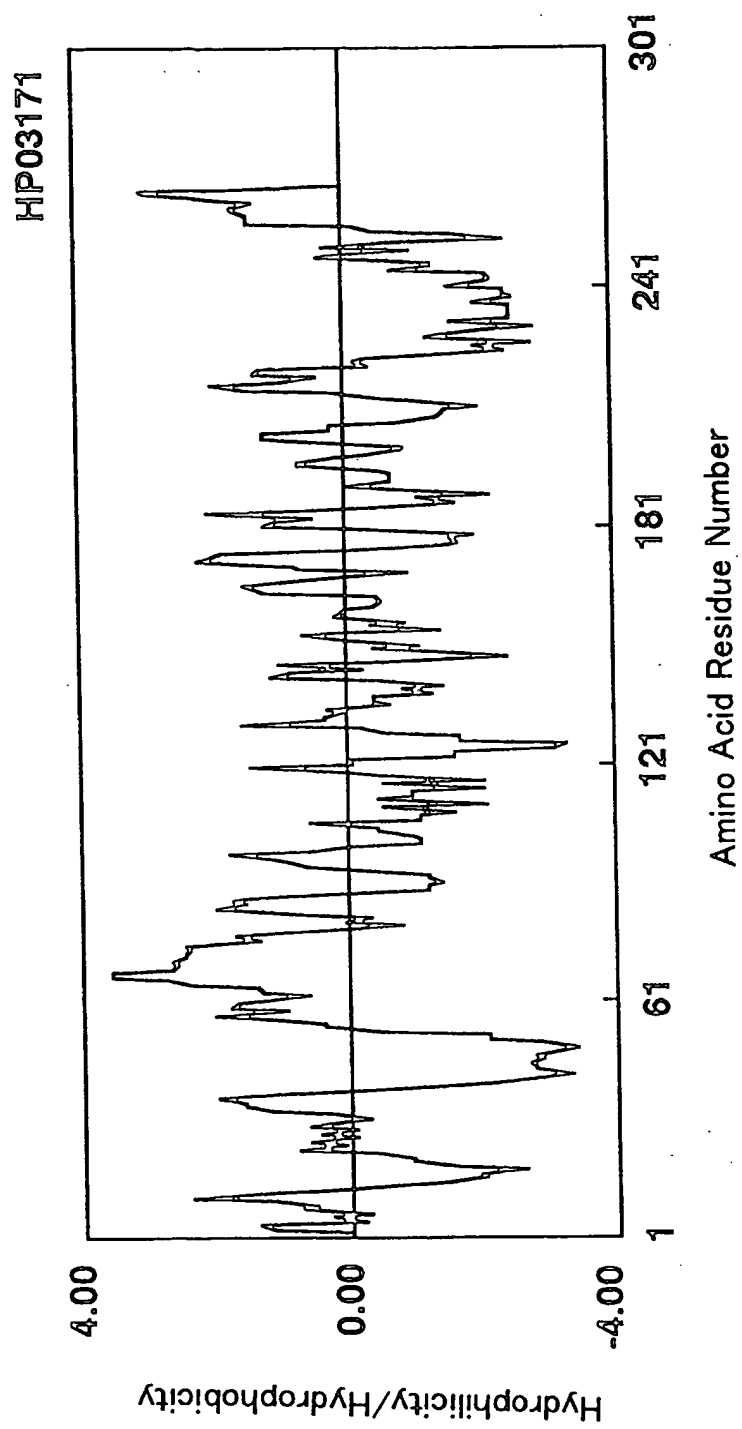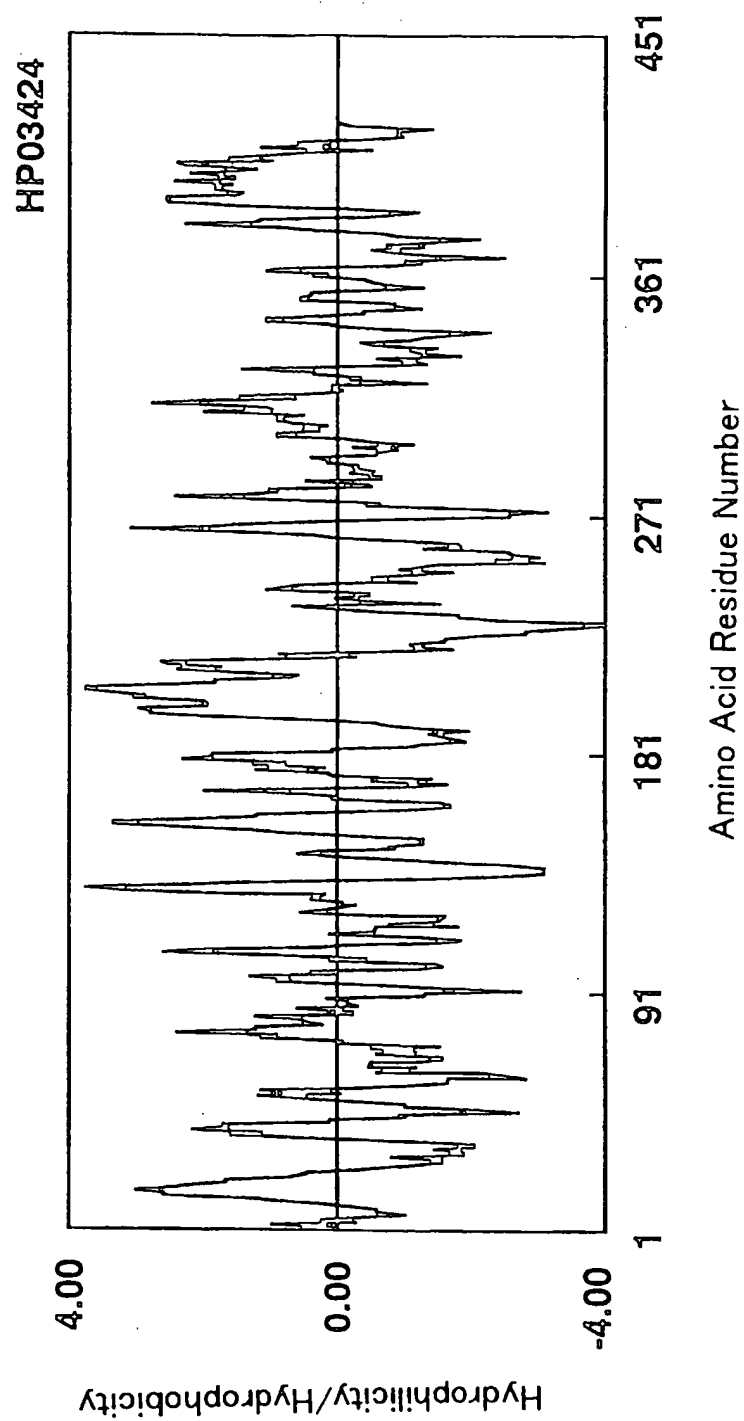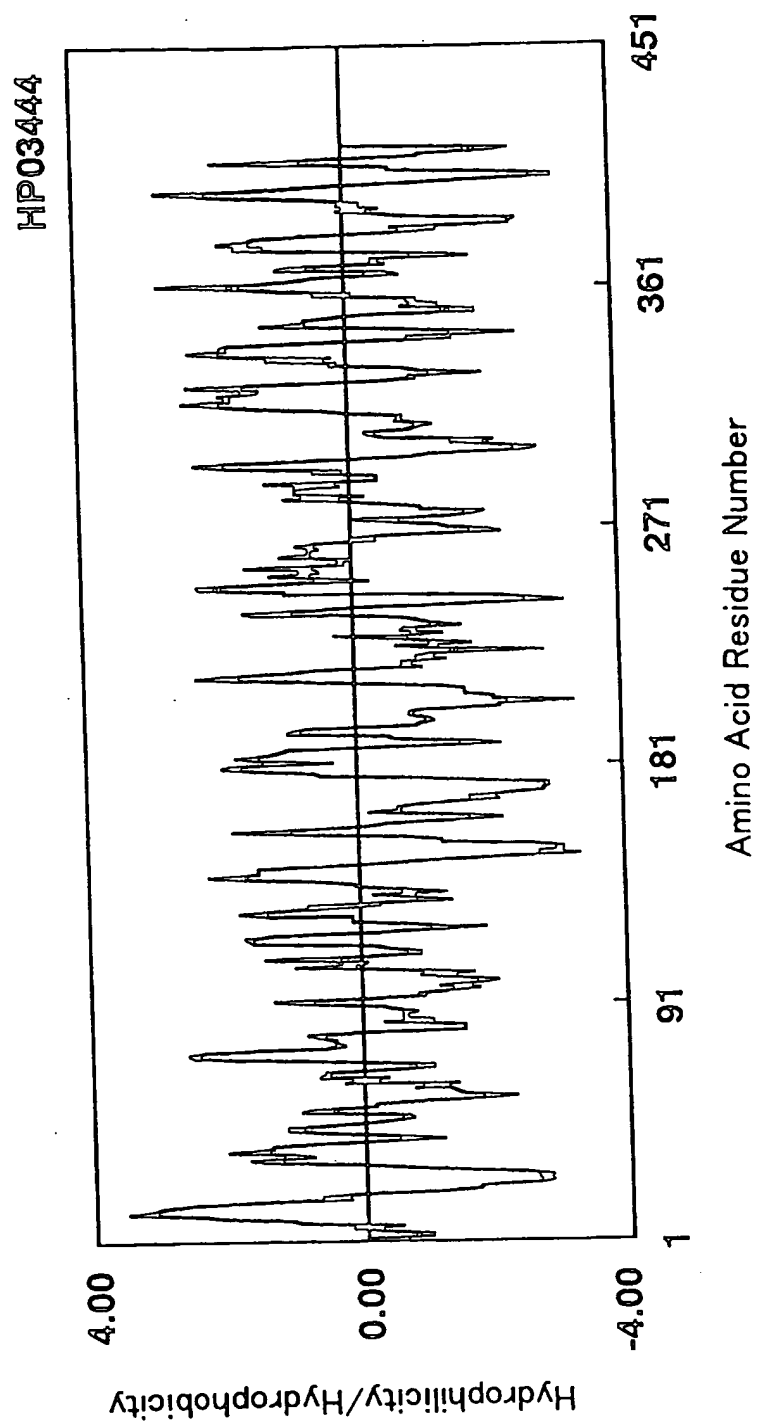
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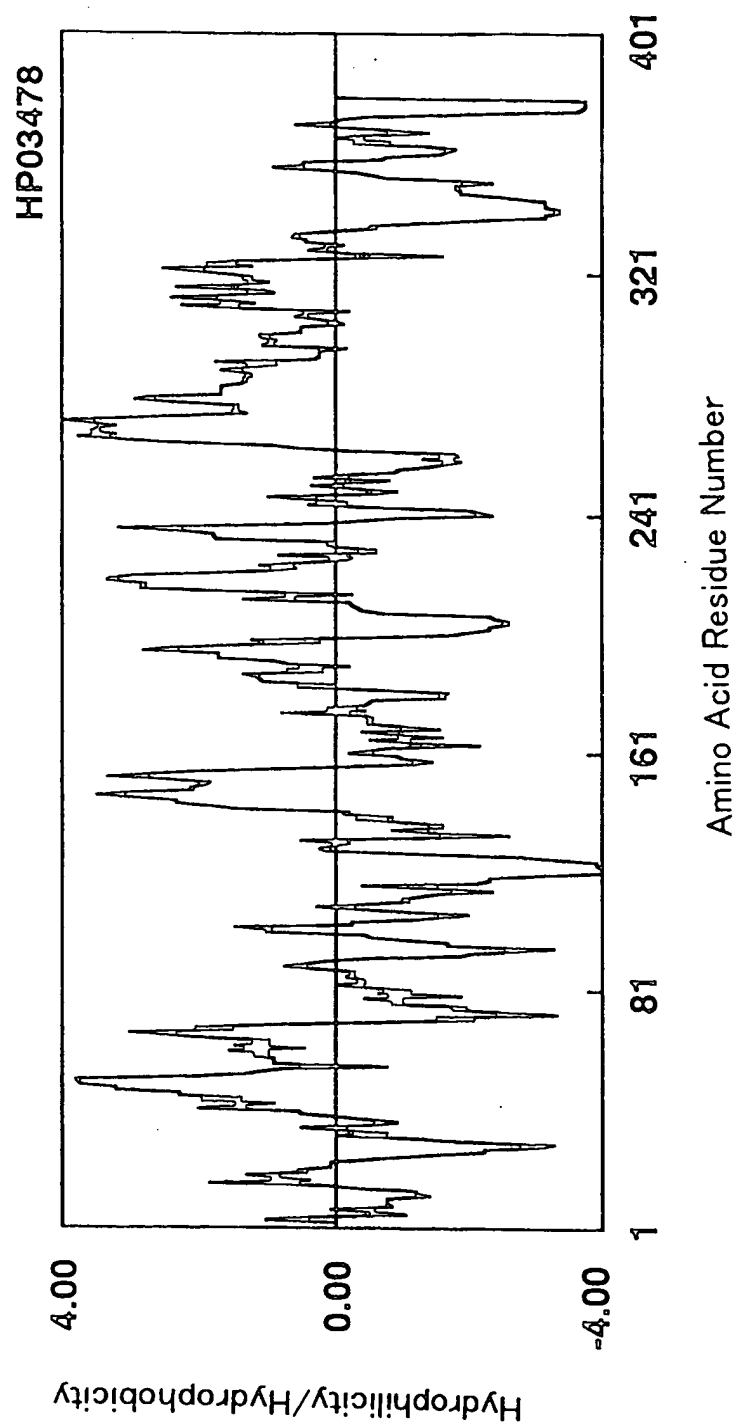
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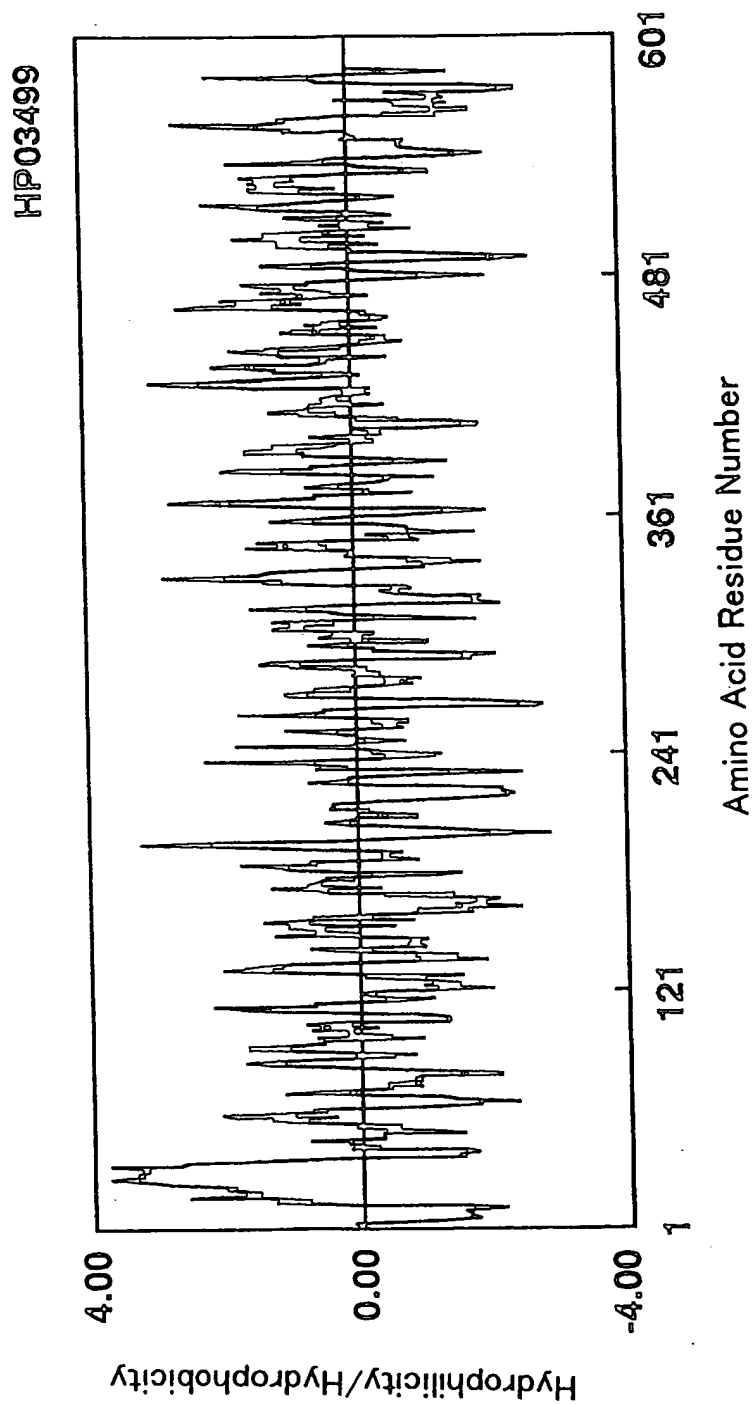
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6/50

Fig.6

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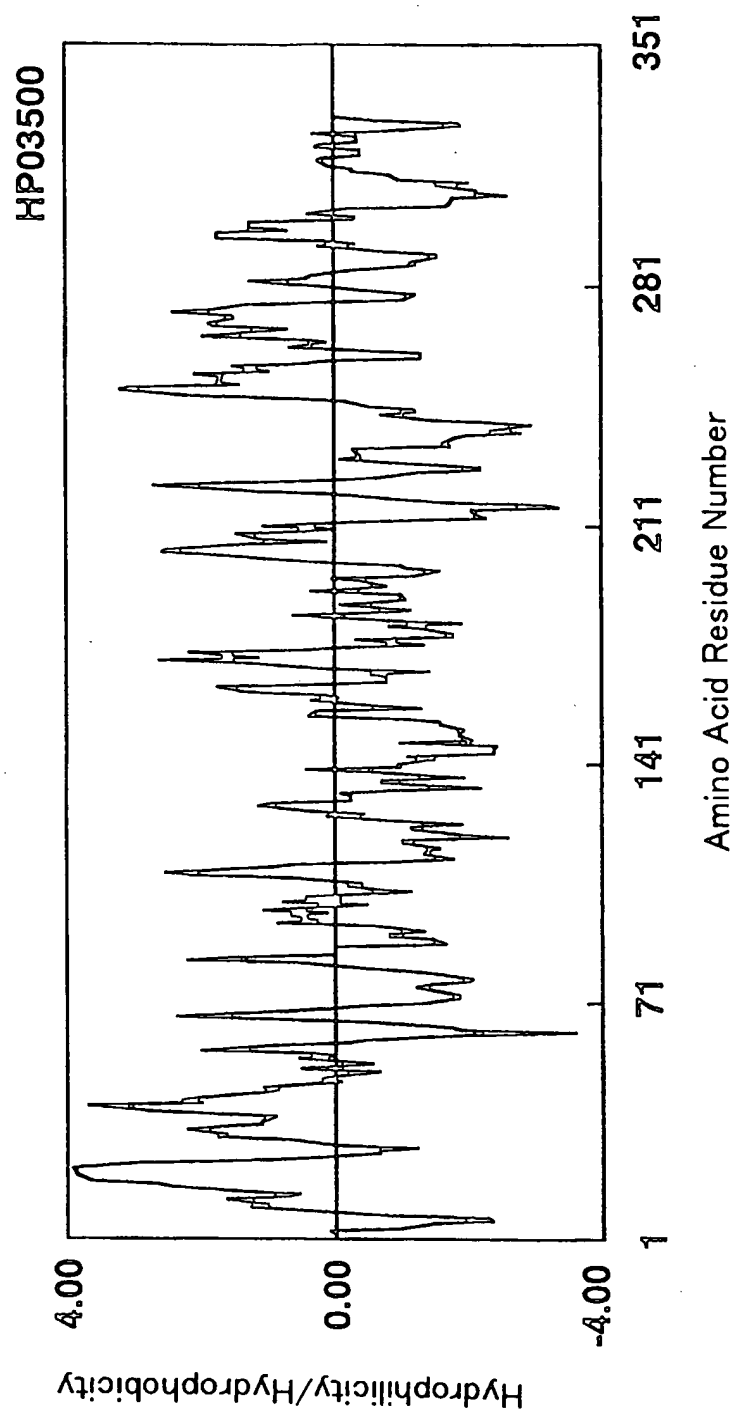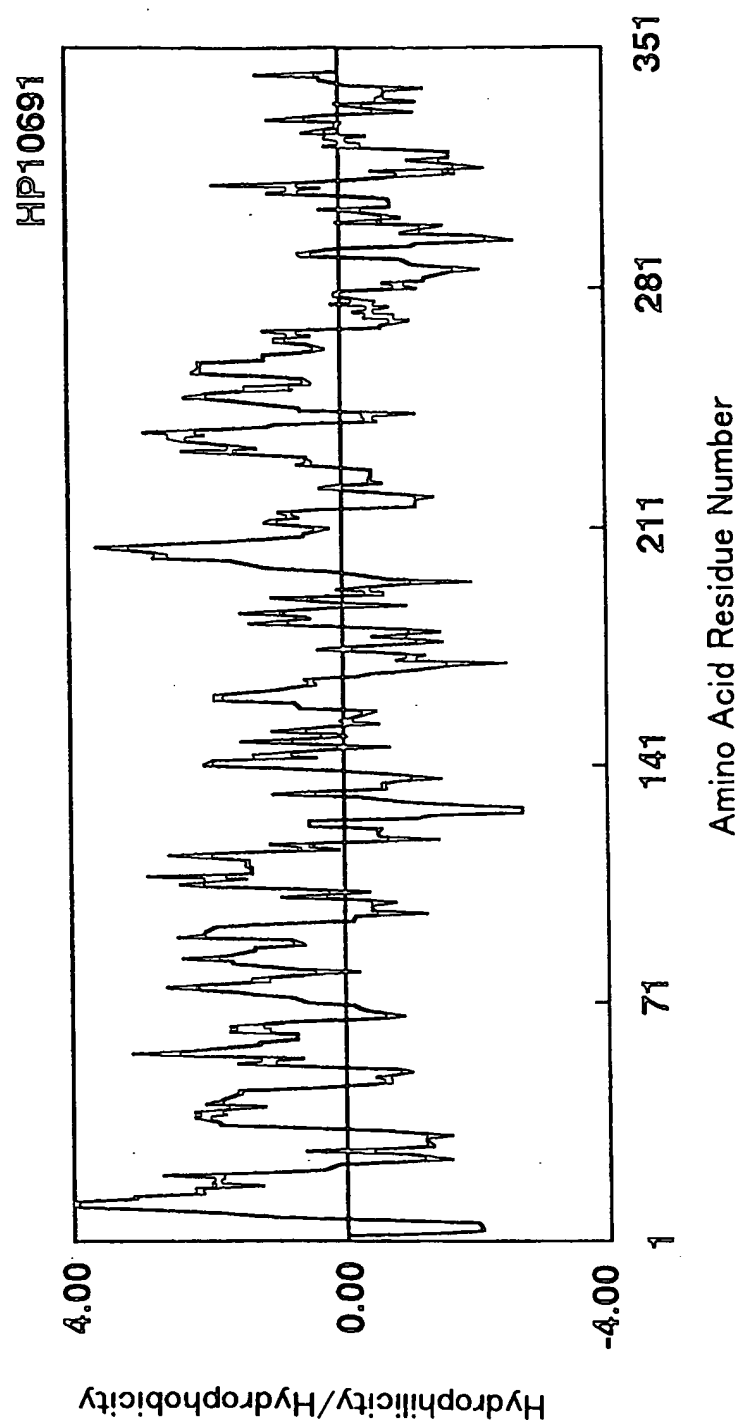
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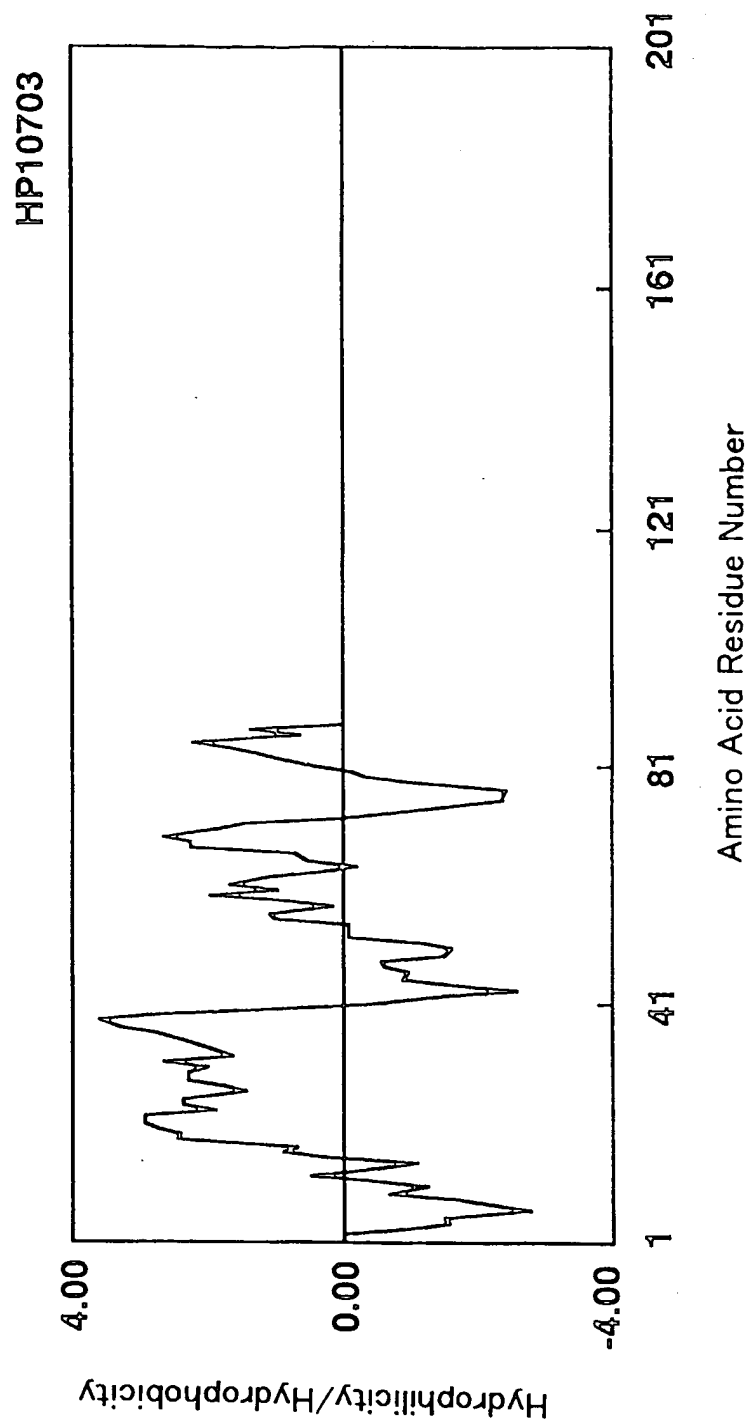
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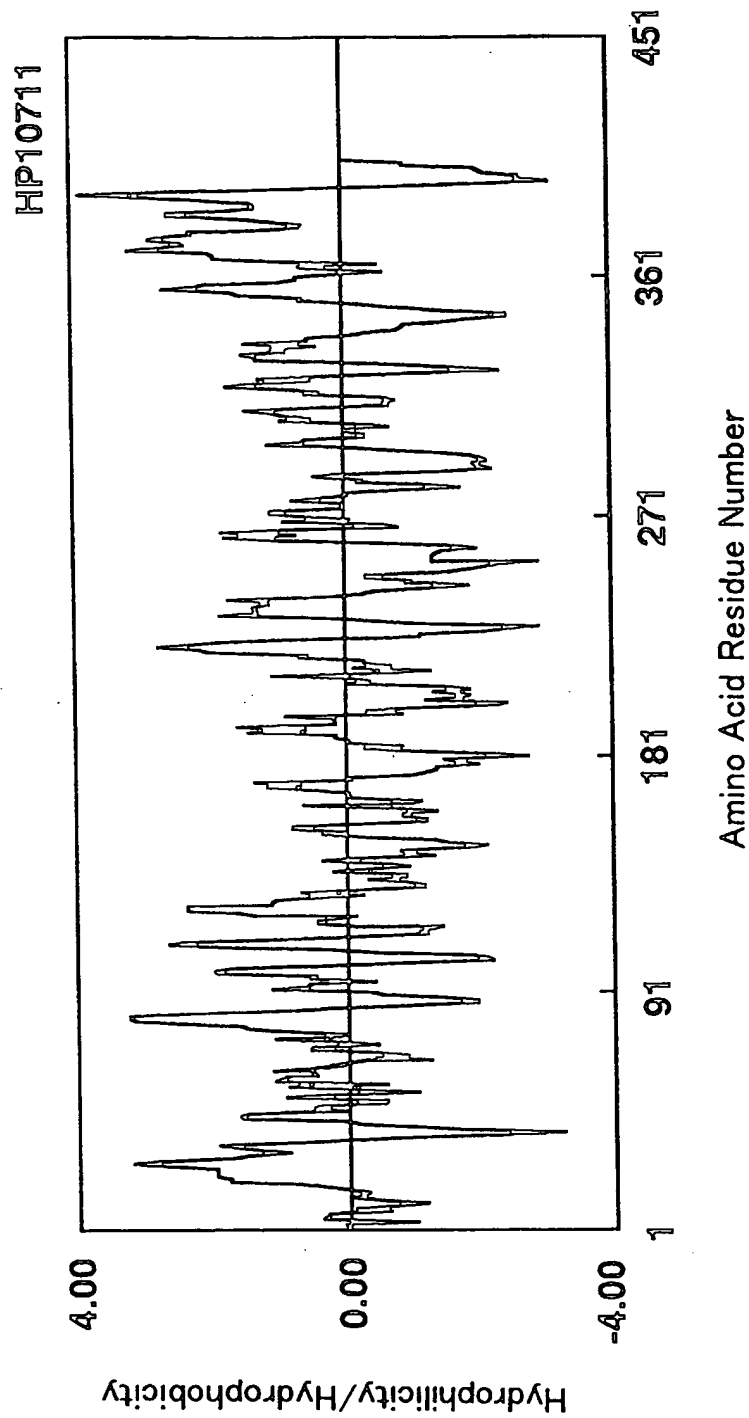
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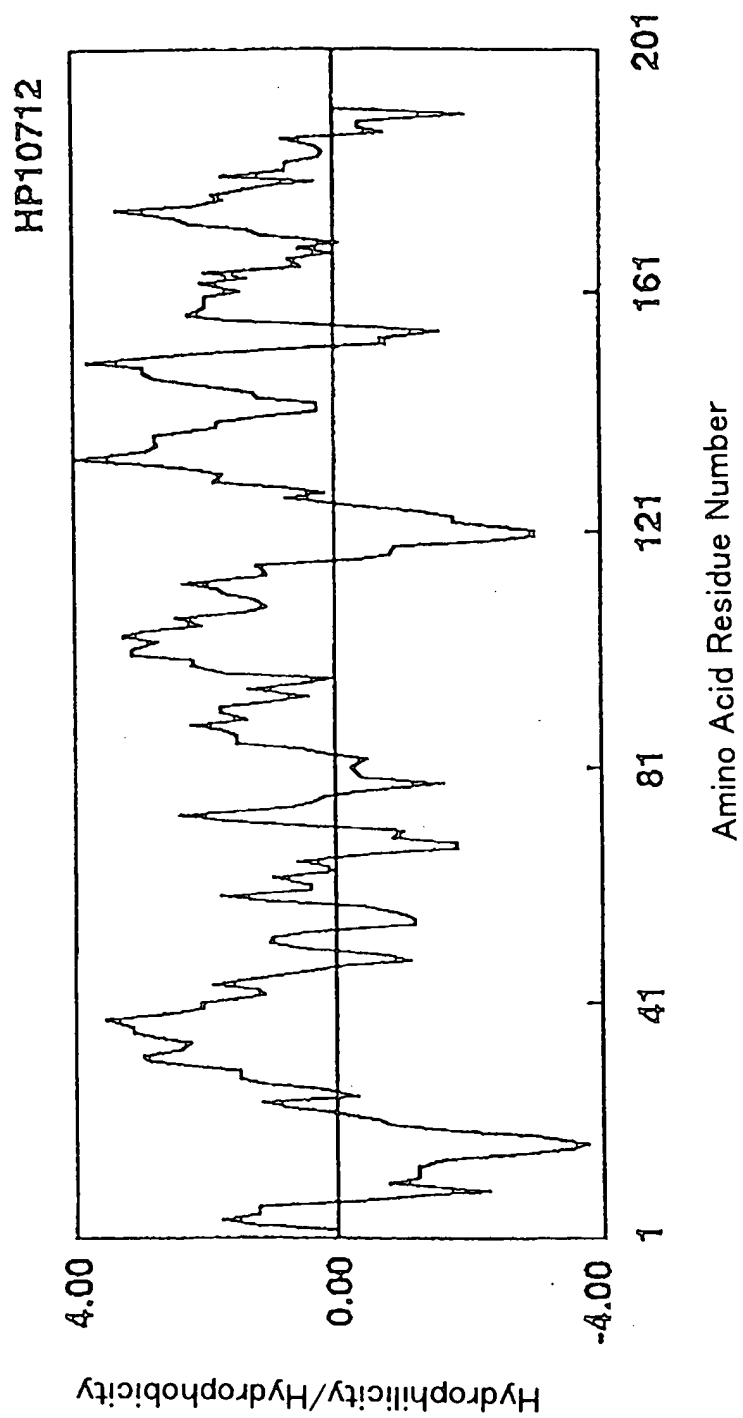
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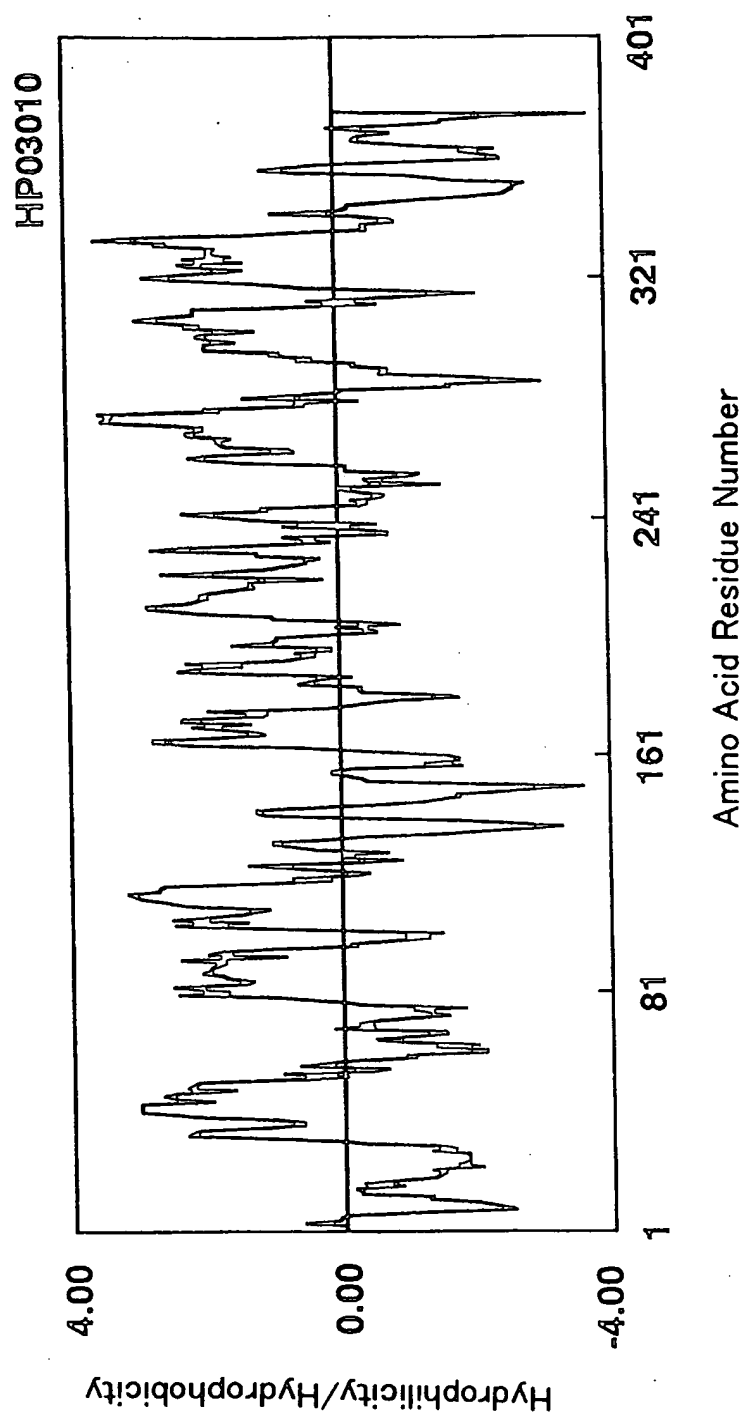
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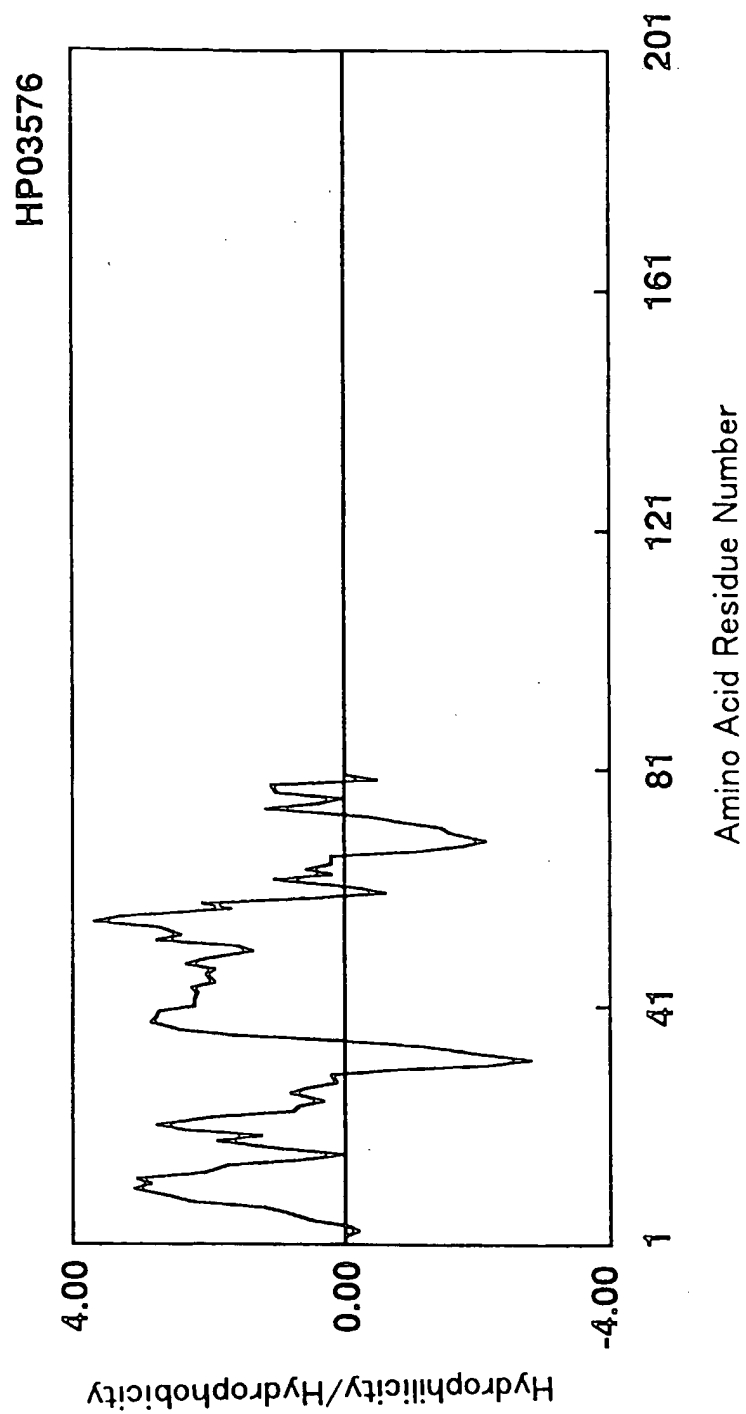
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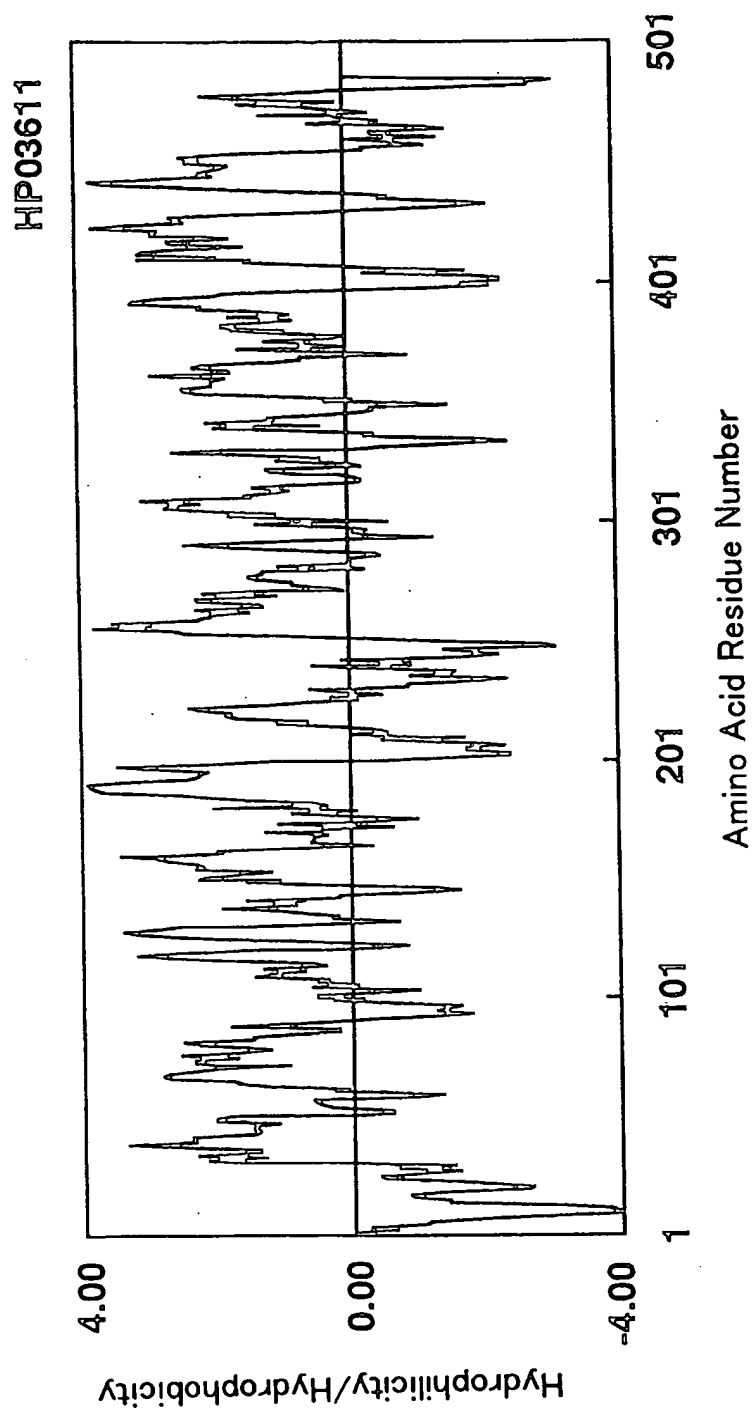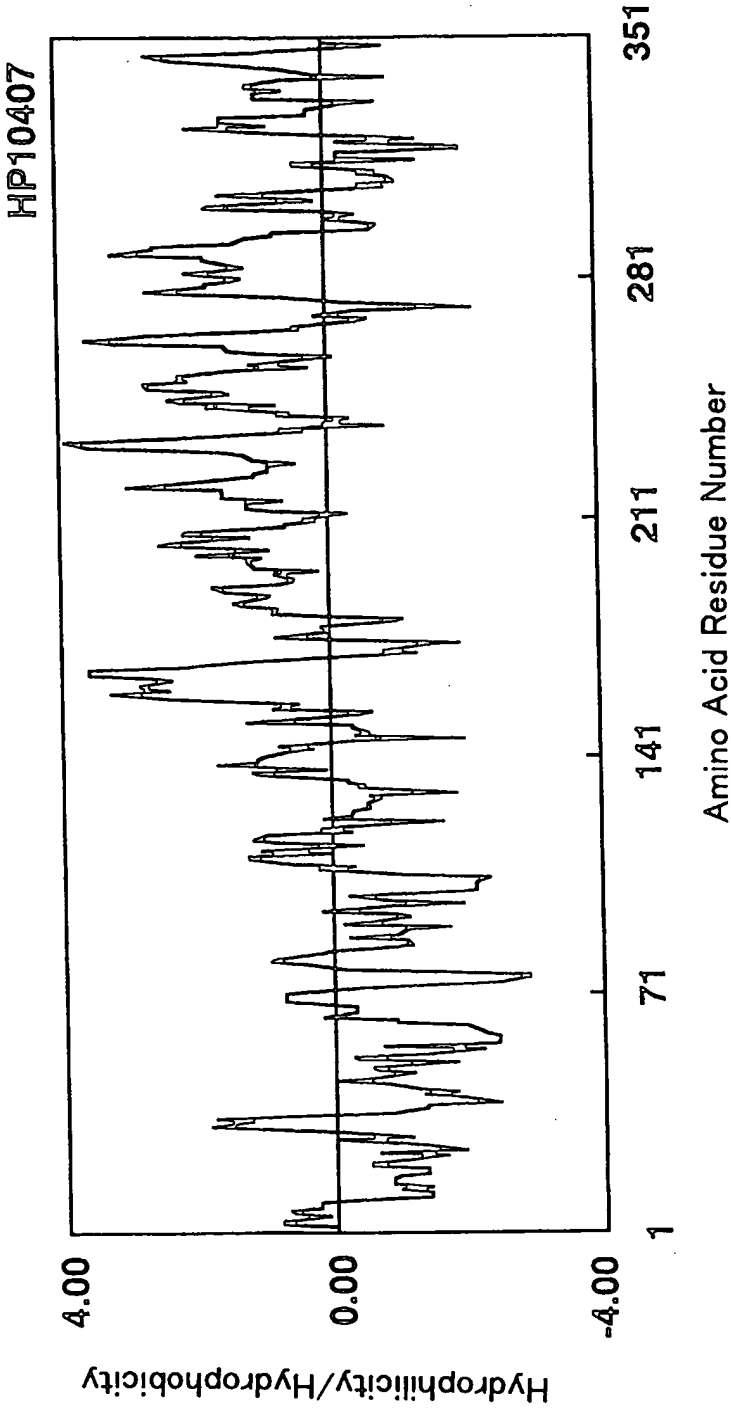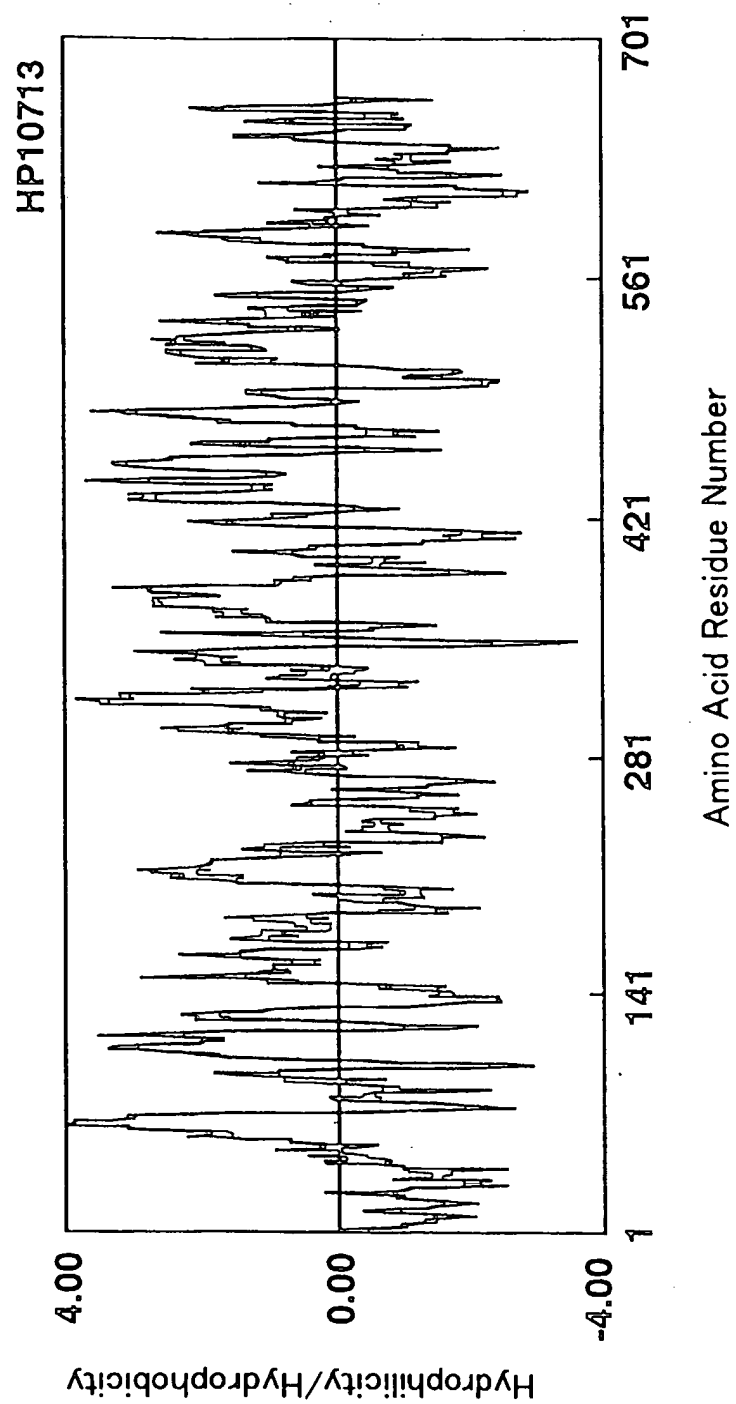
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Fig.14

Fig.15

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Fig.16
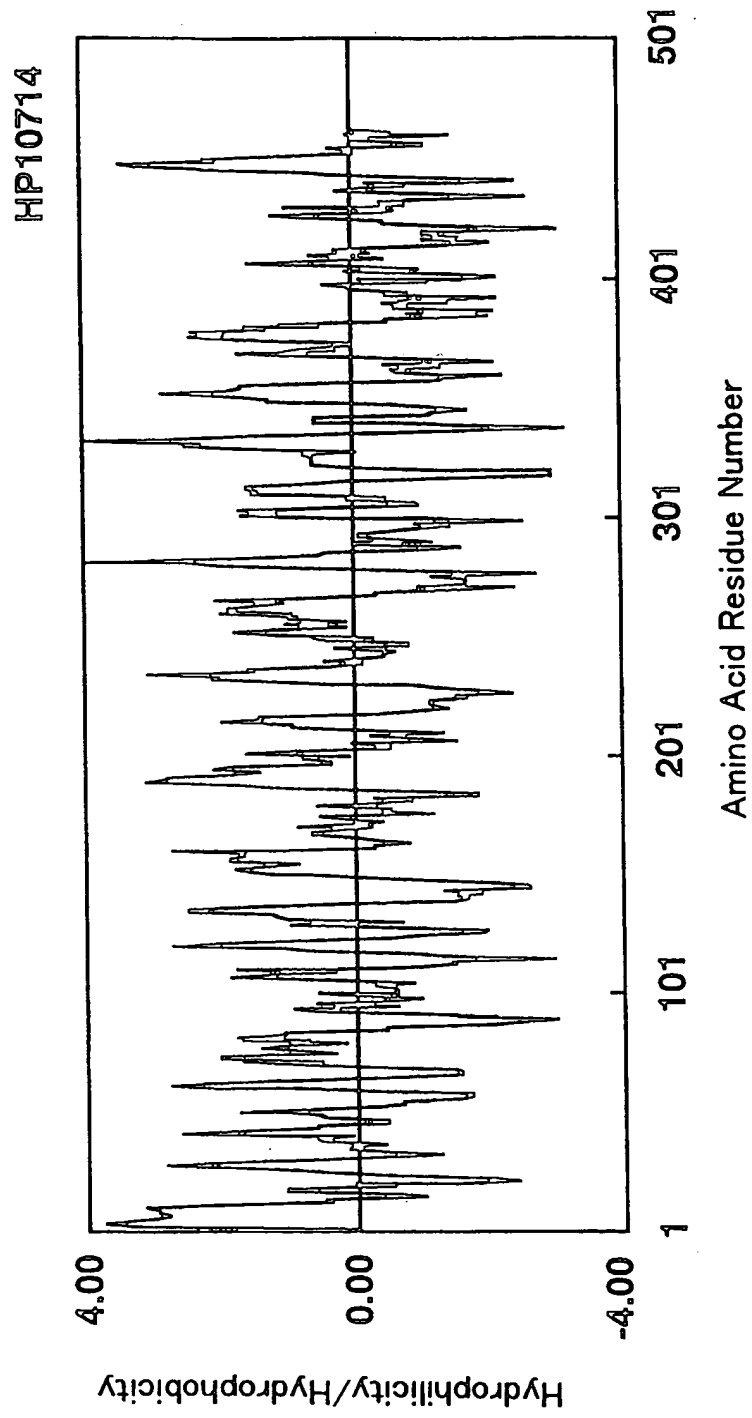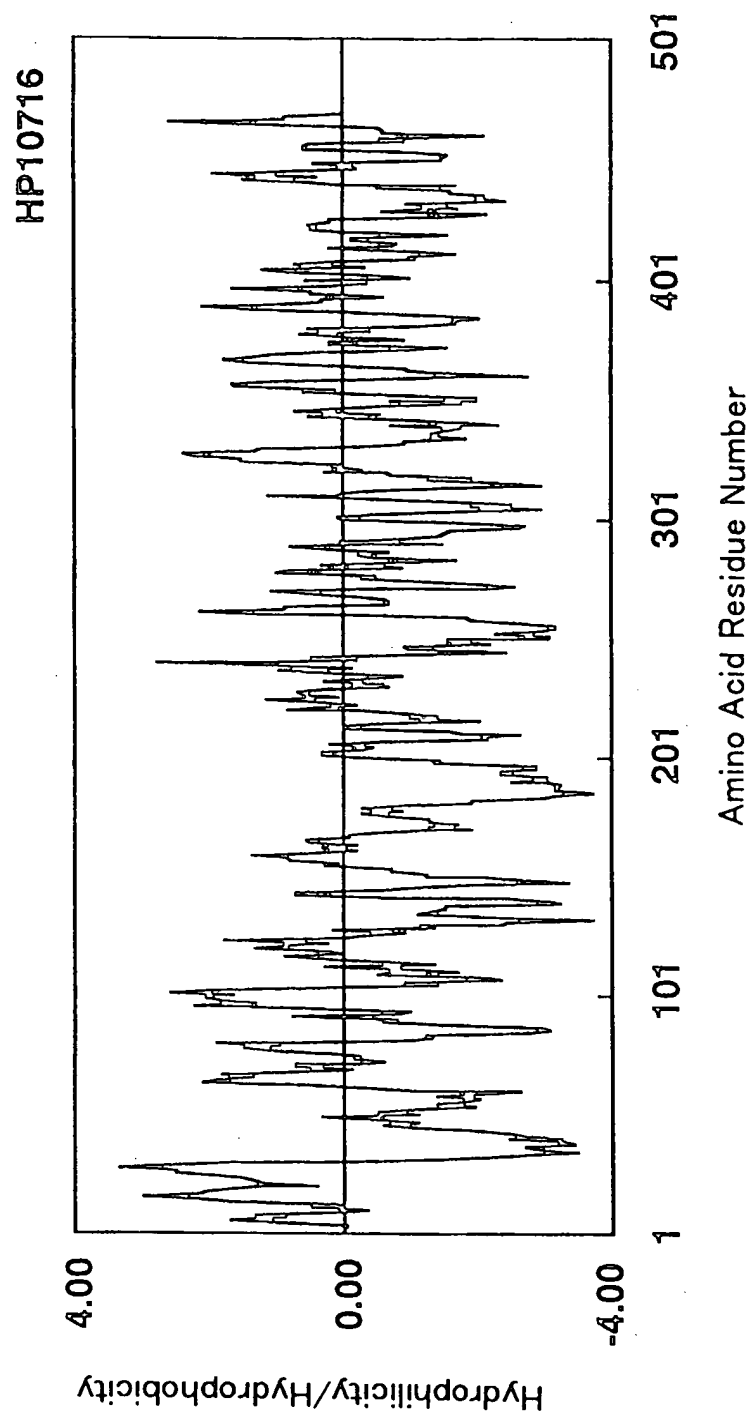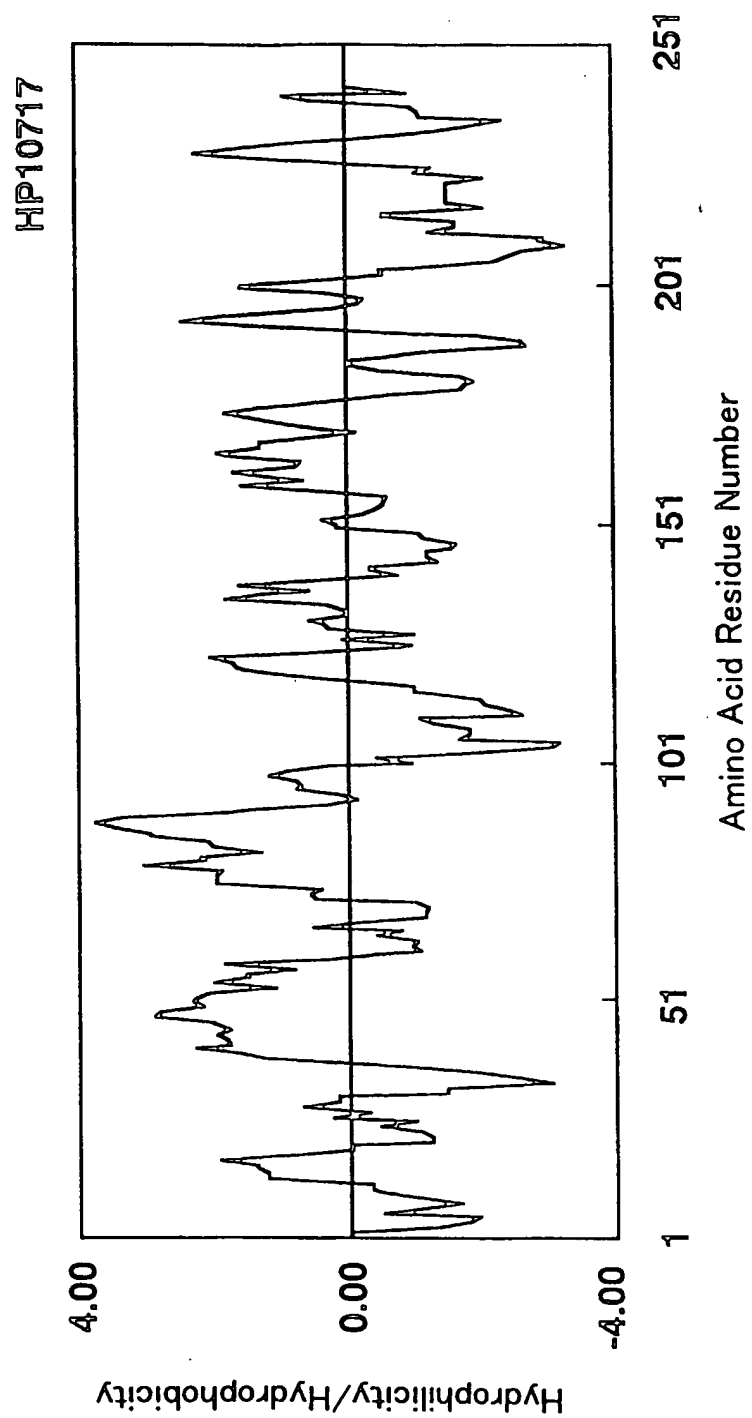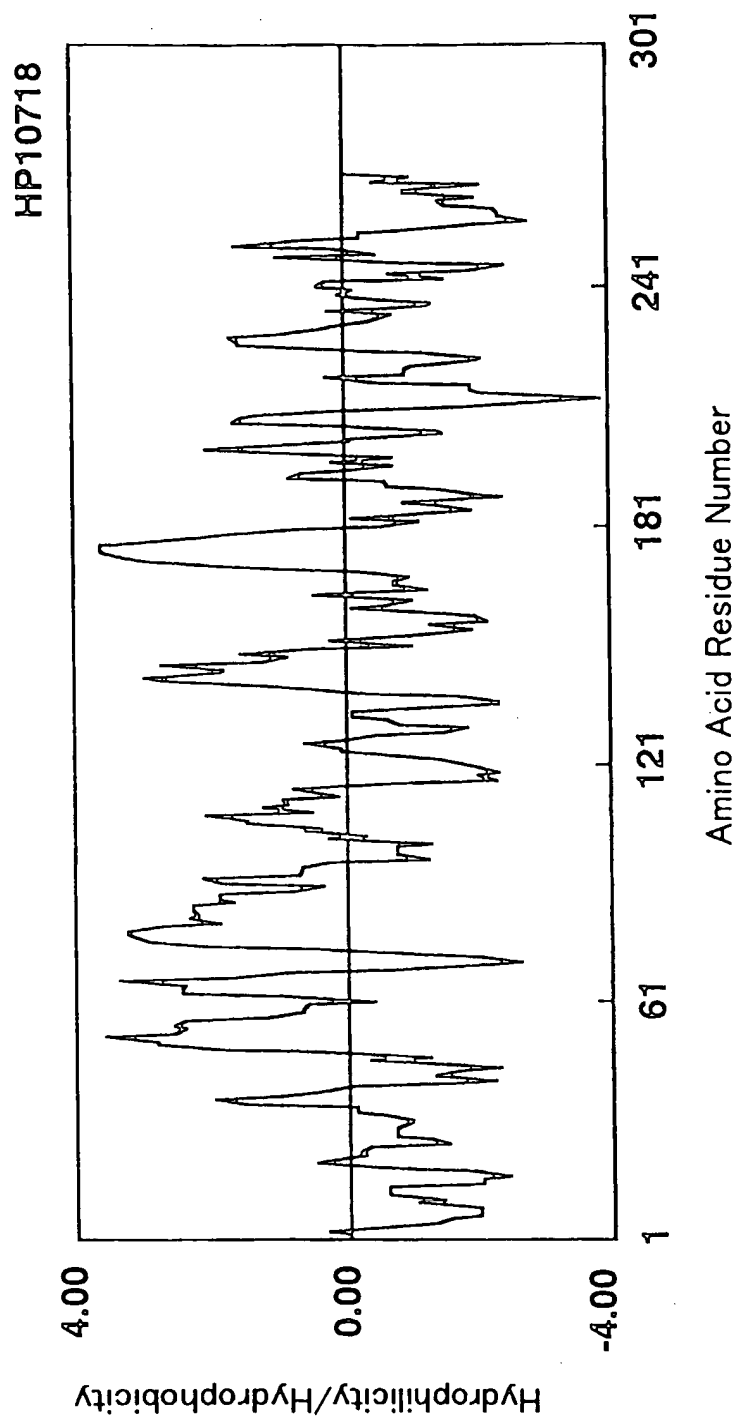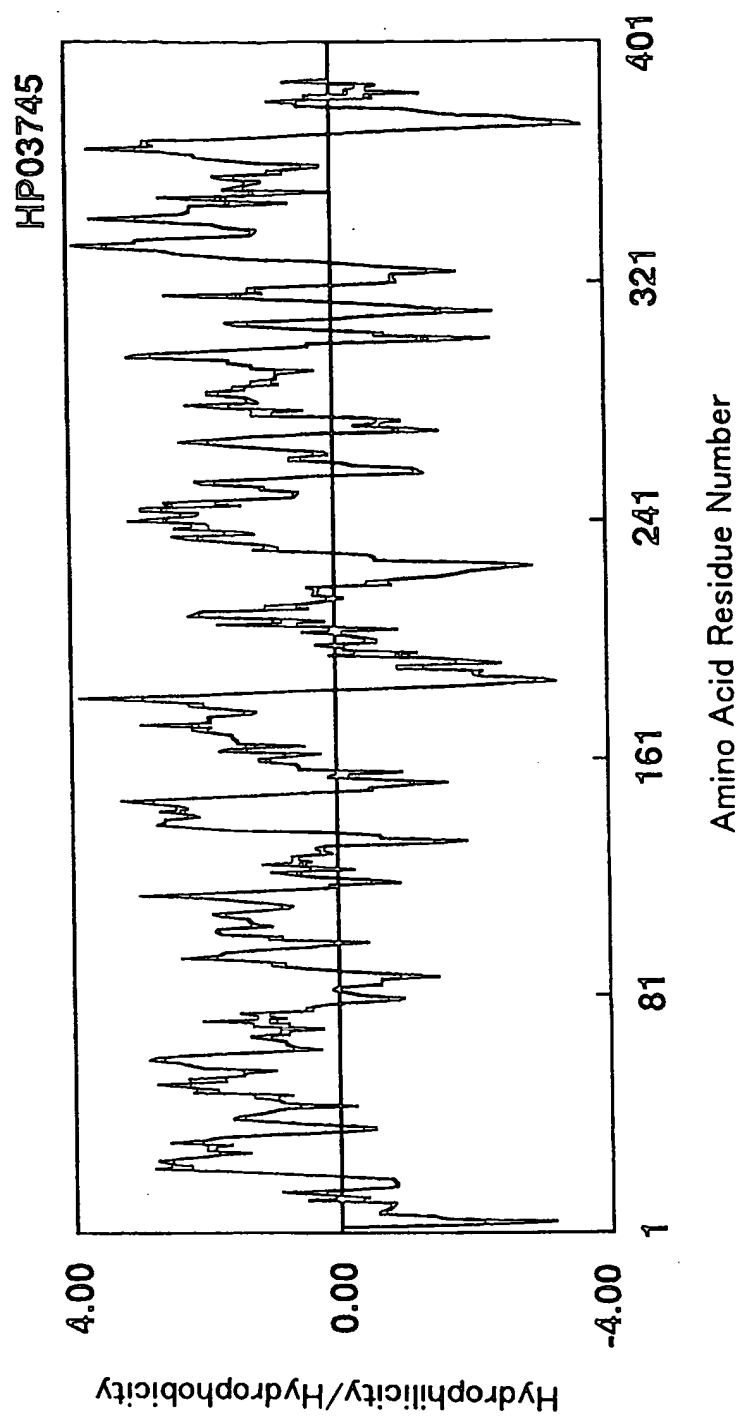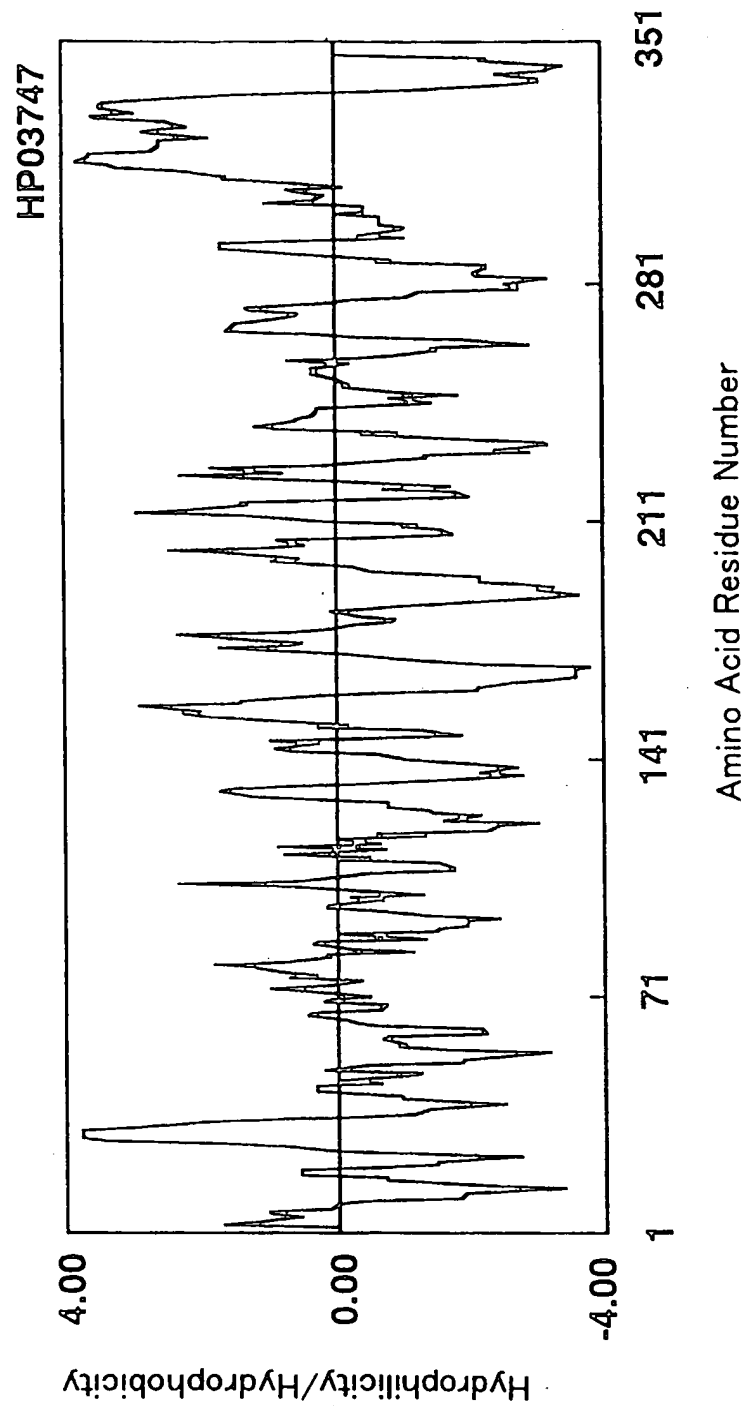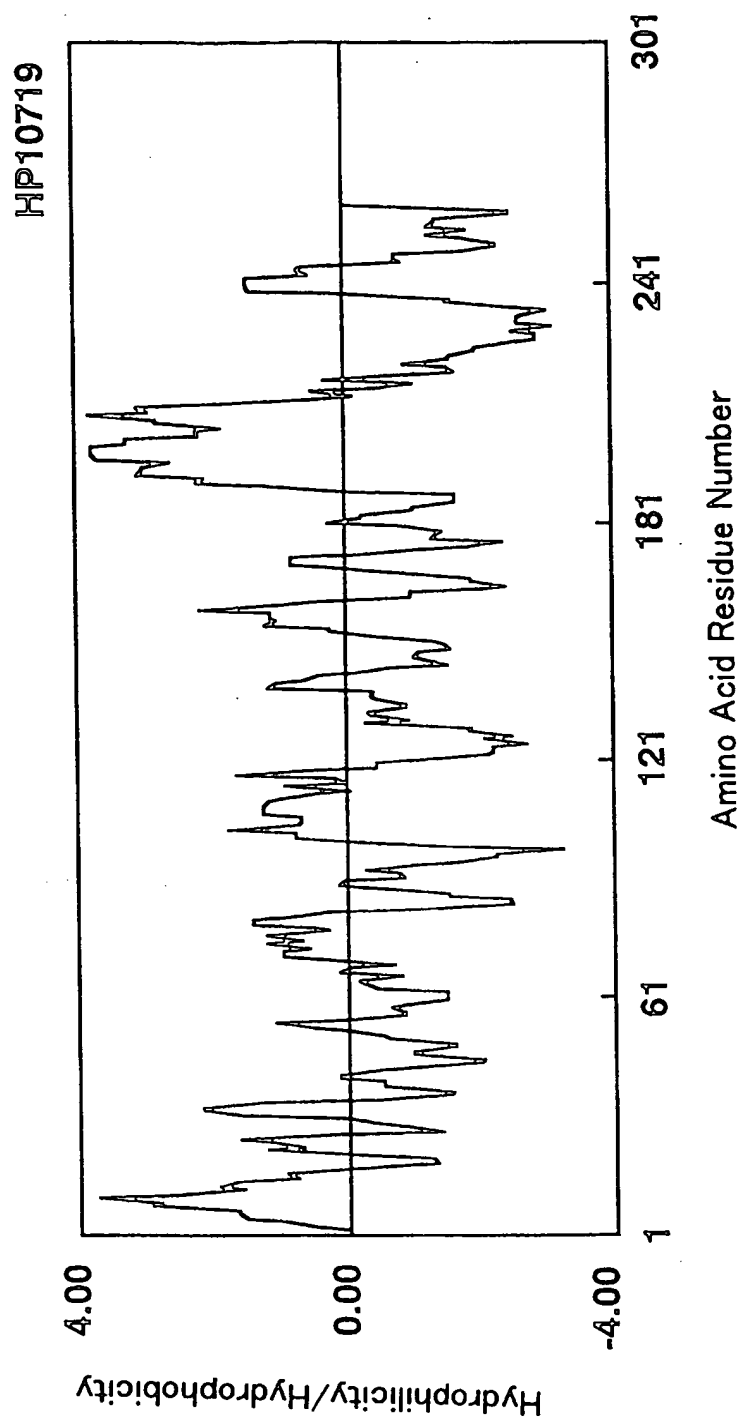
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Fig.18

Fig.19

Fig.20

Fig.21

Fig.22

23/50

Fig.23
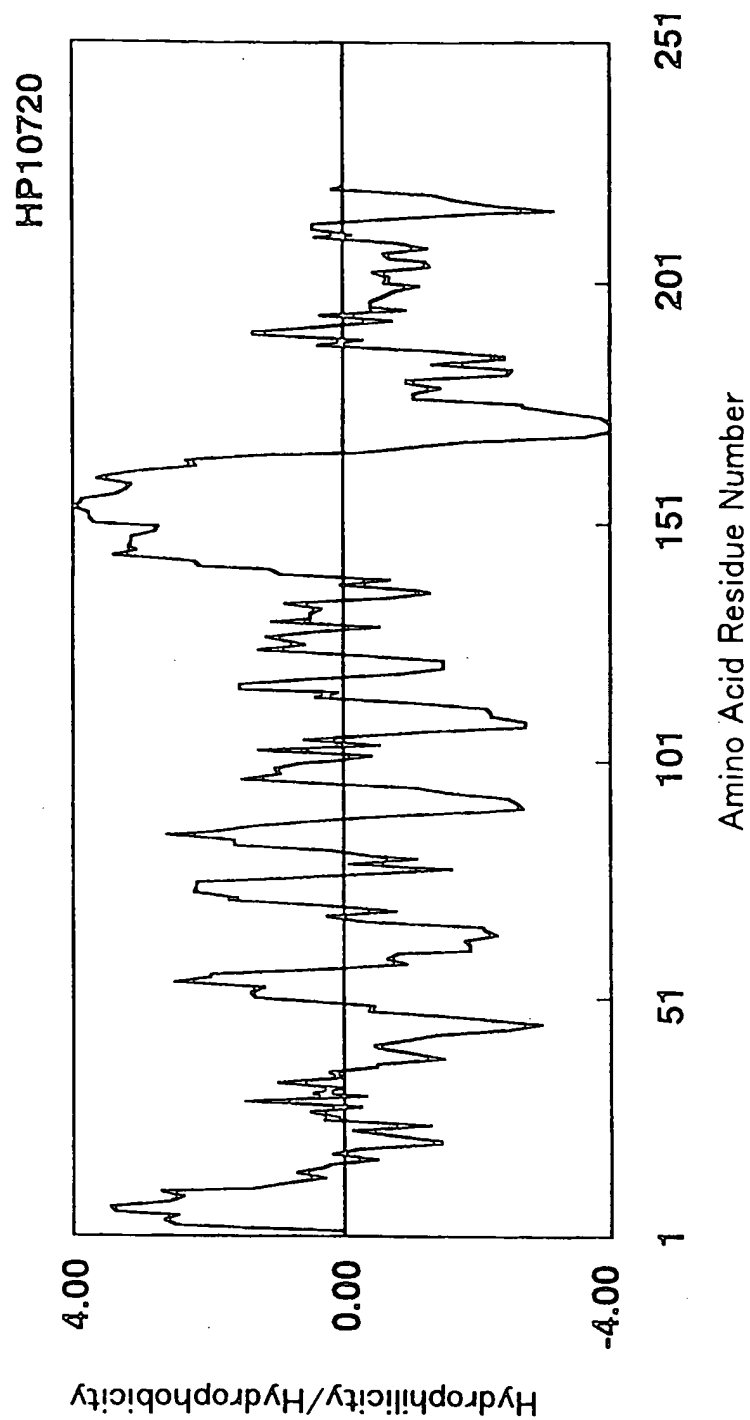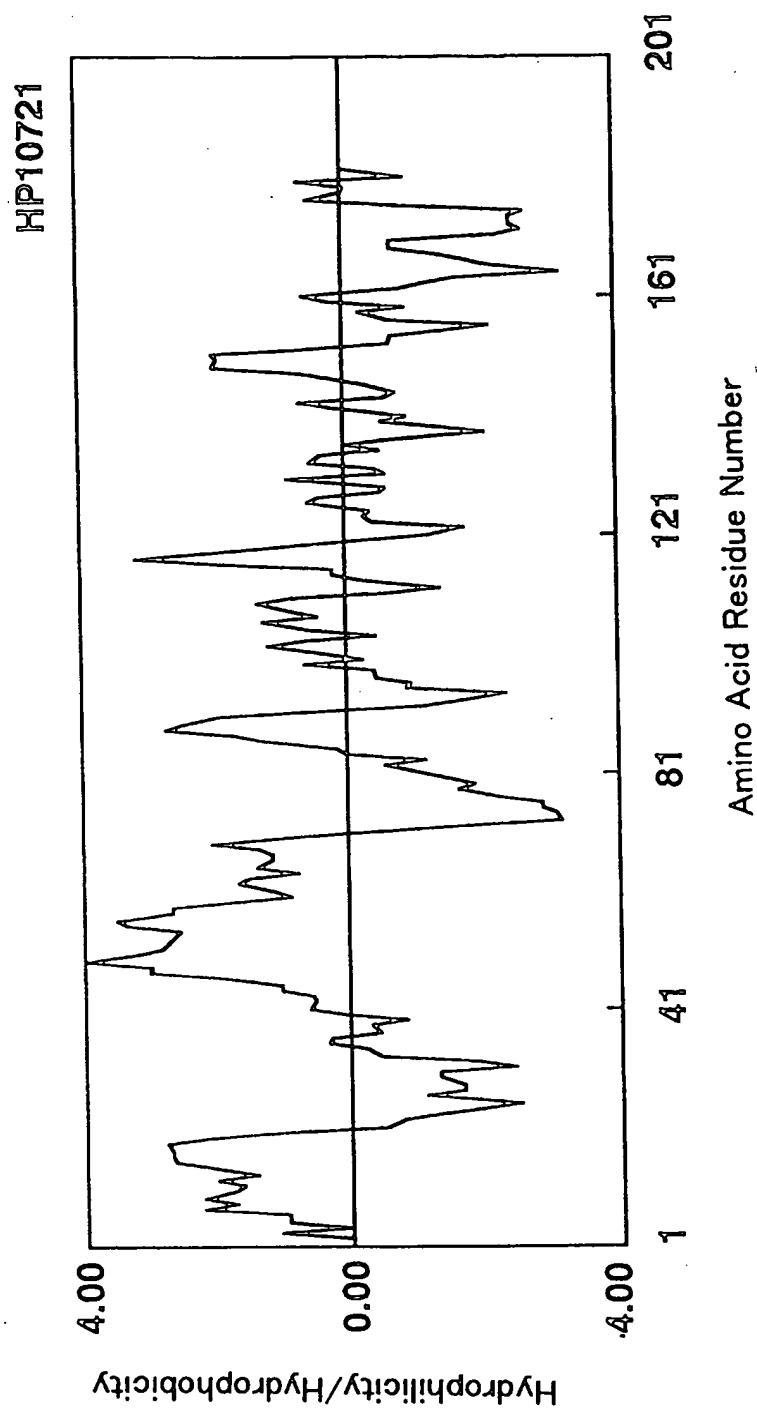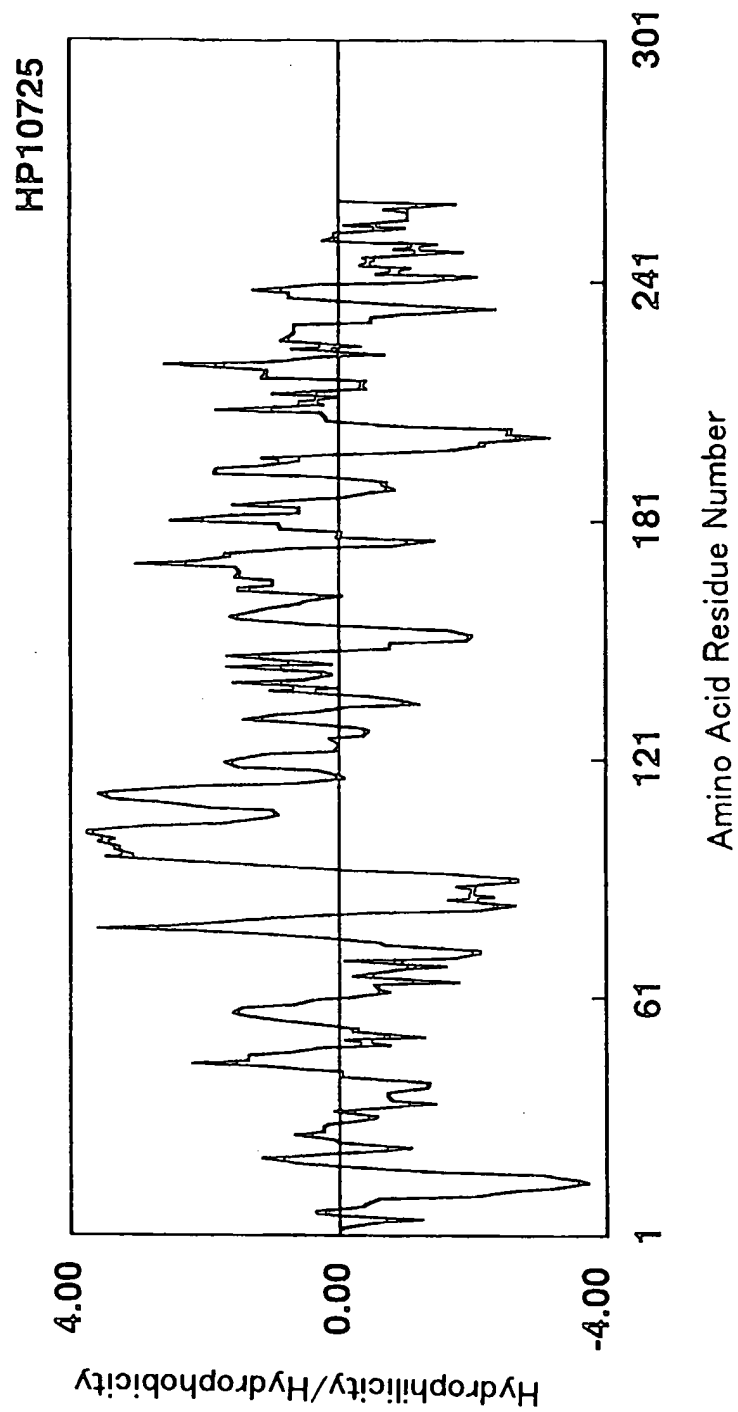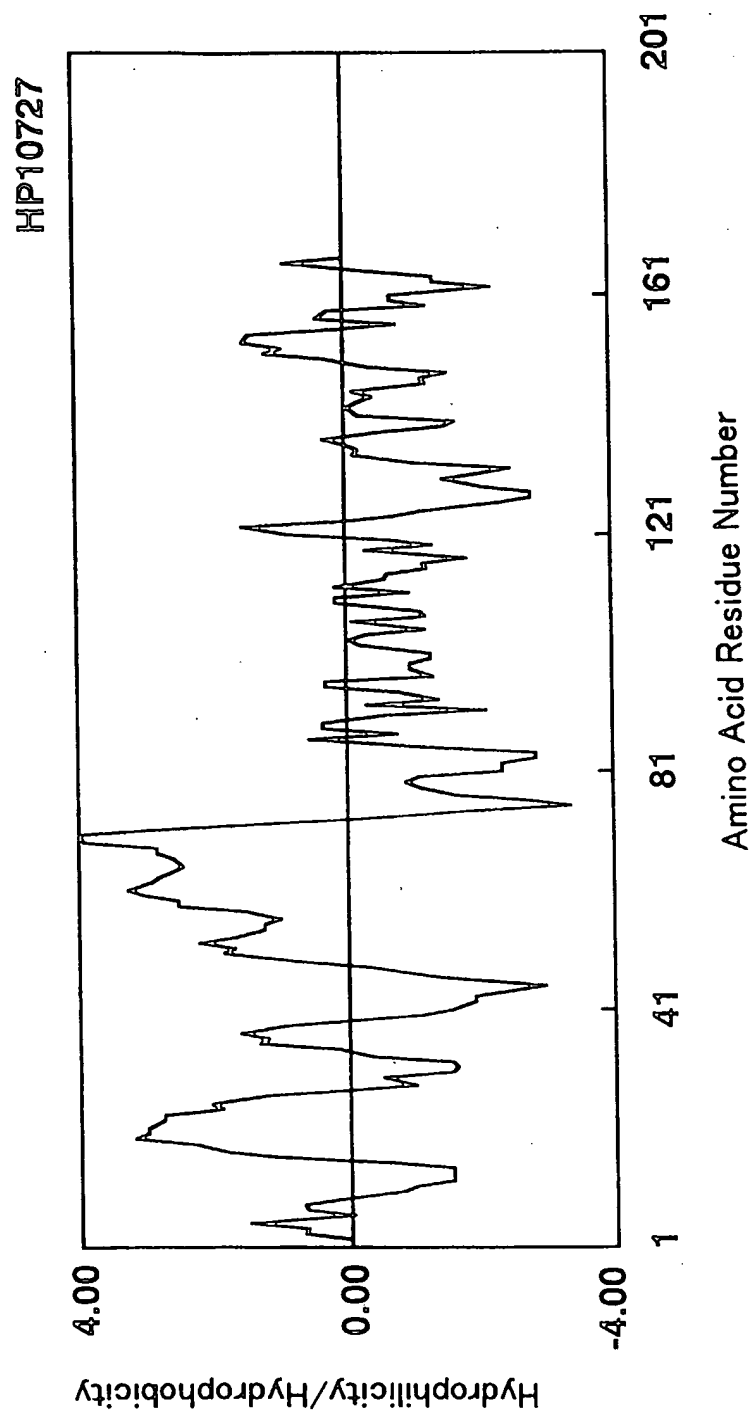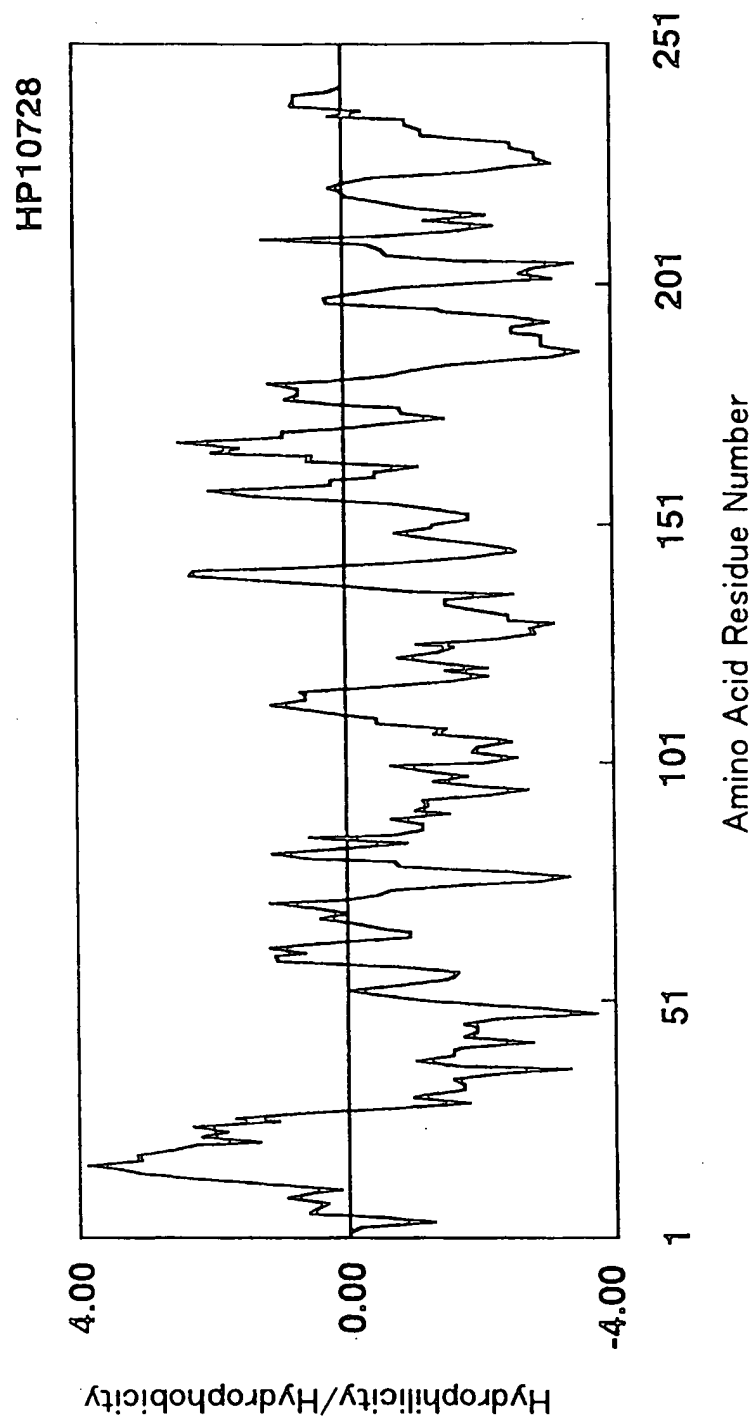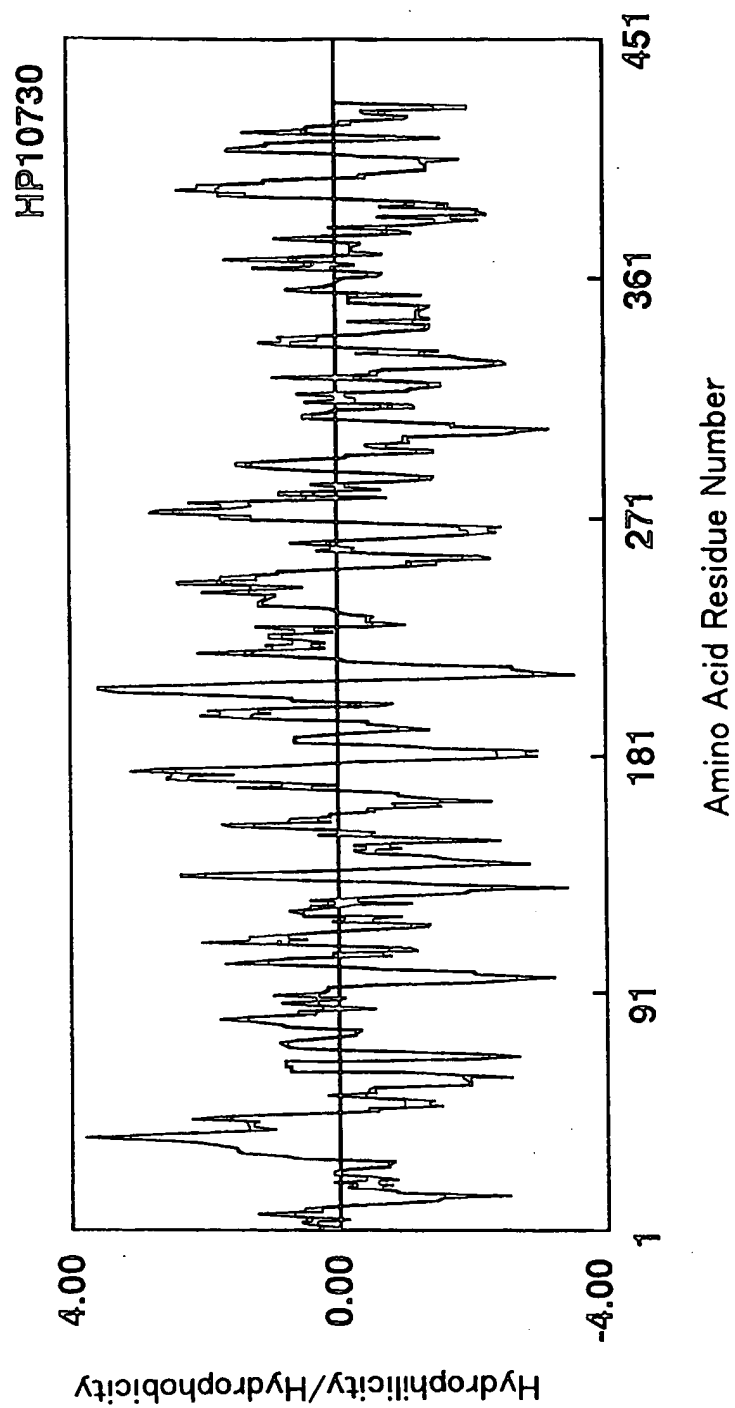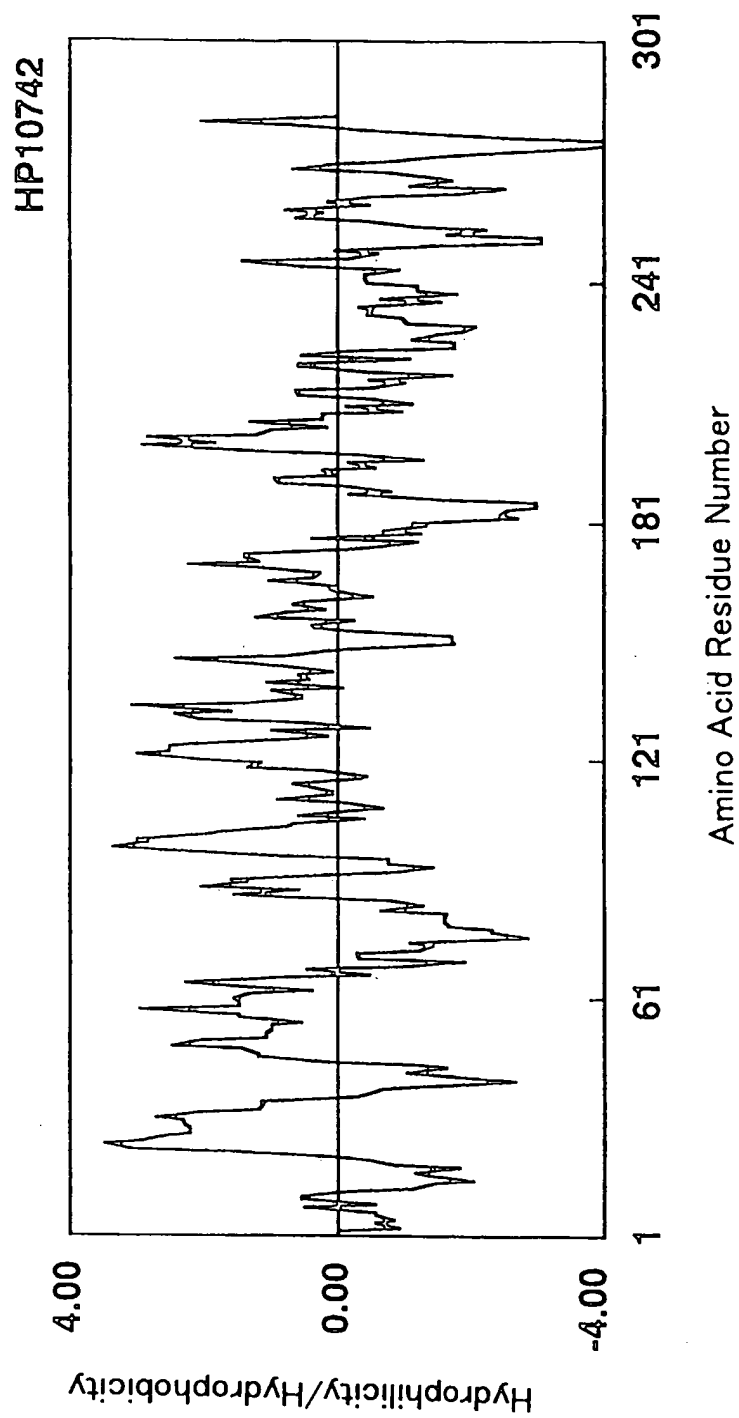
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Fig.25

Fig.26

Fig.27

Fig.28

Fig.29

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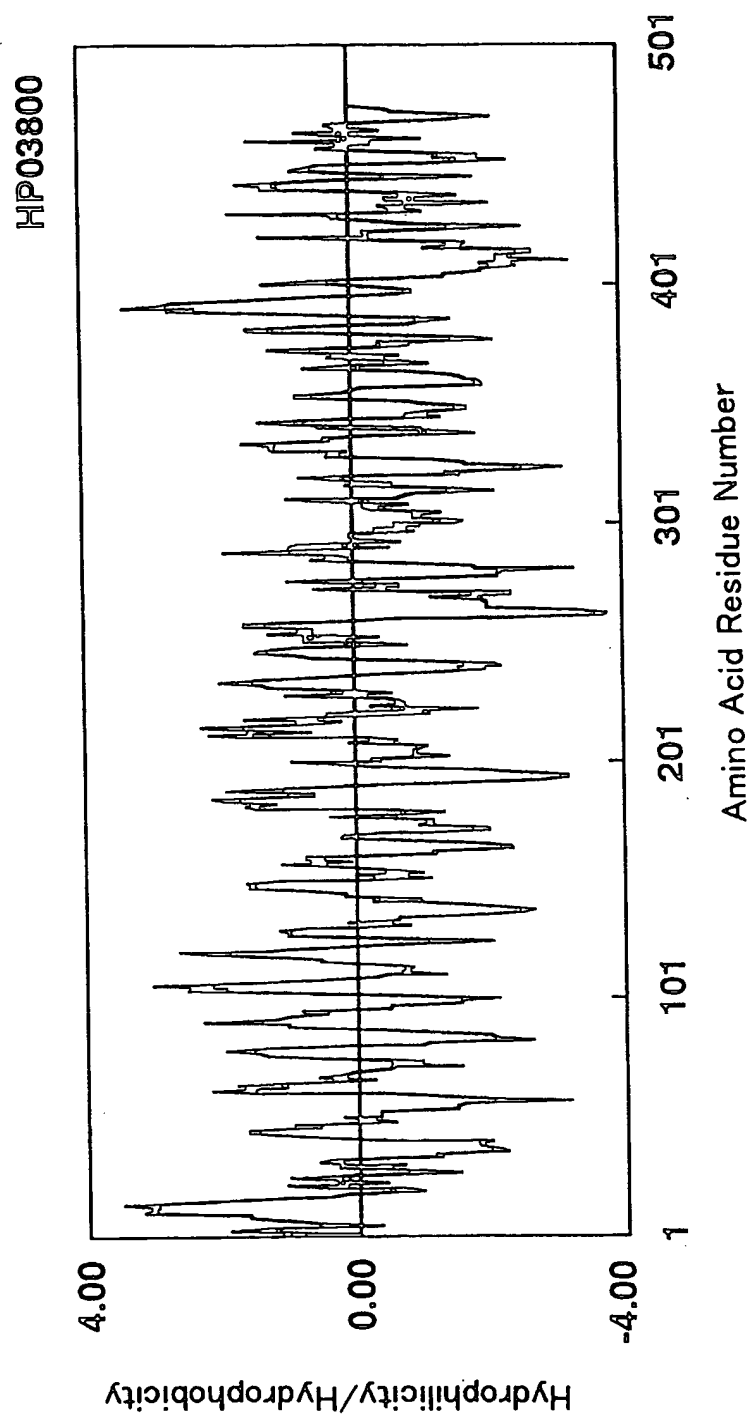
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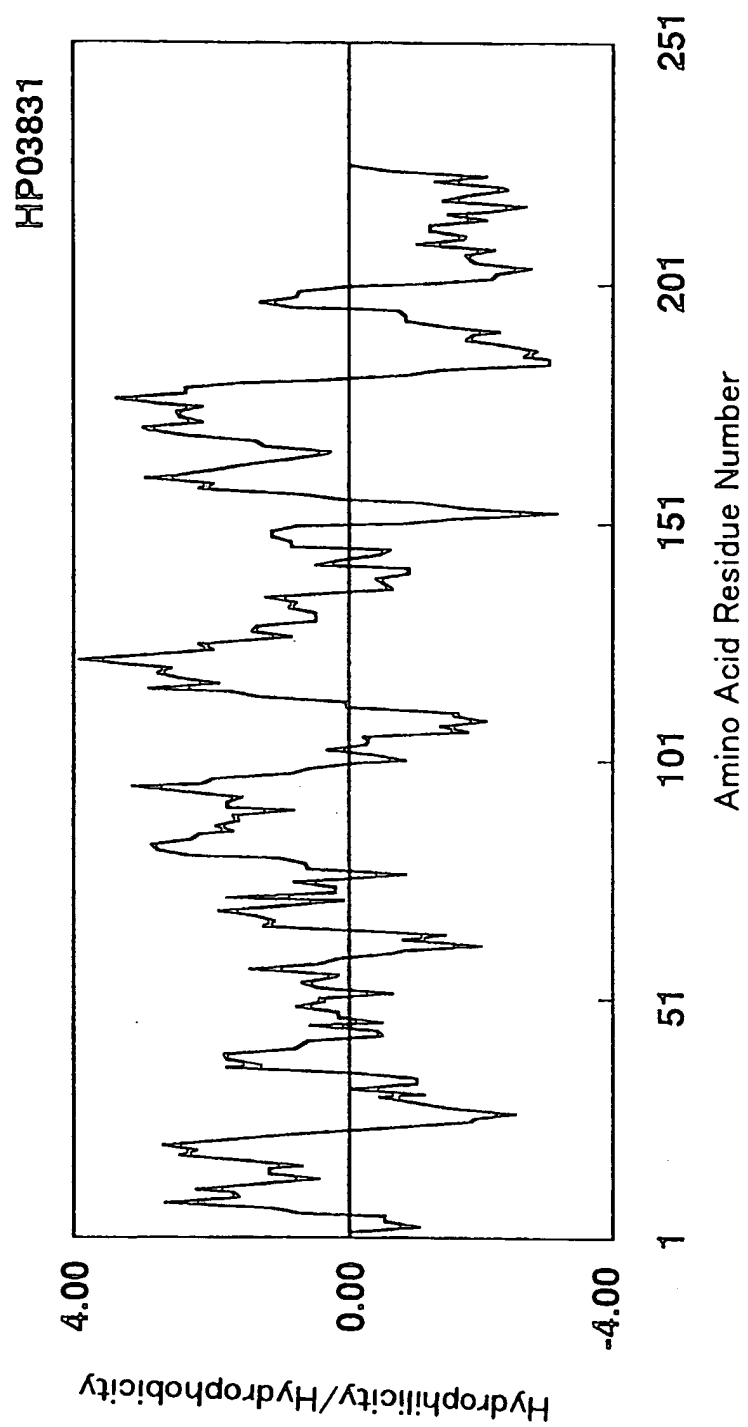
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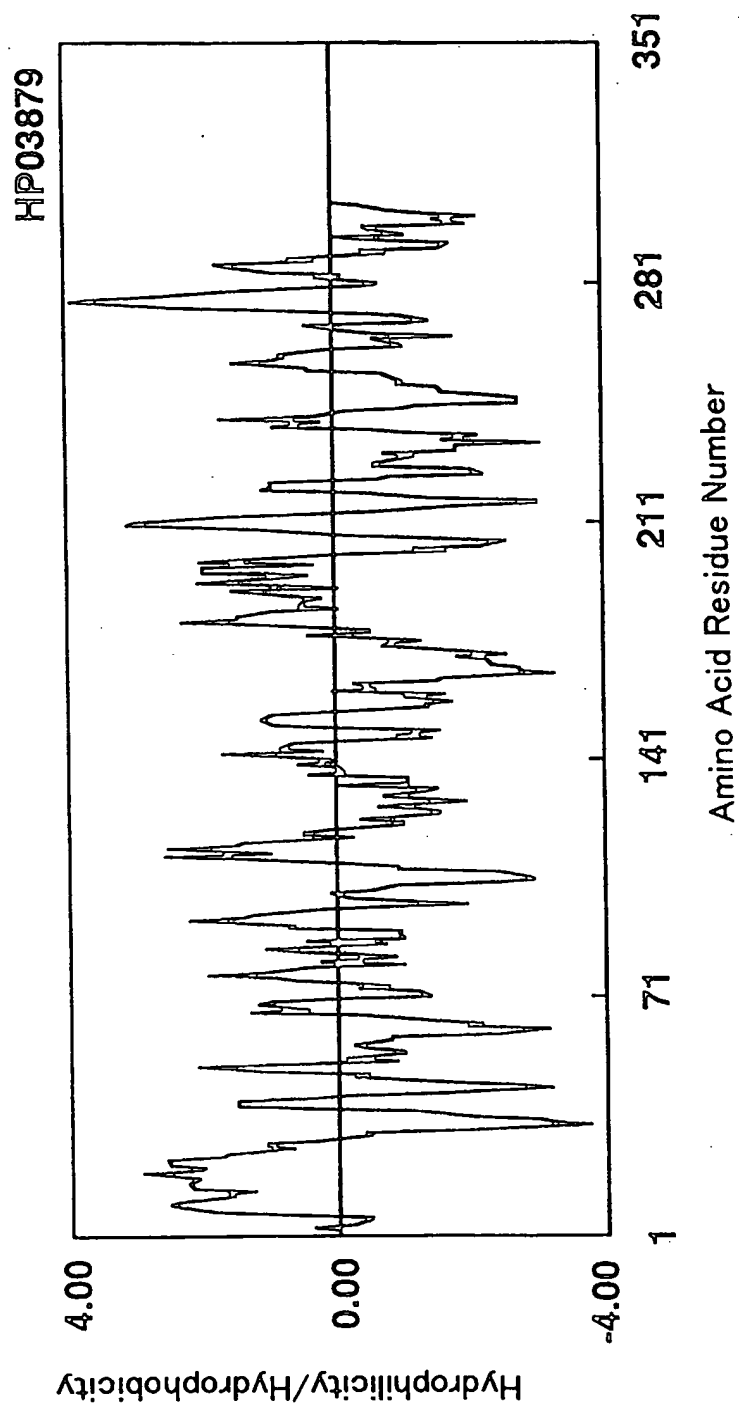
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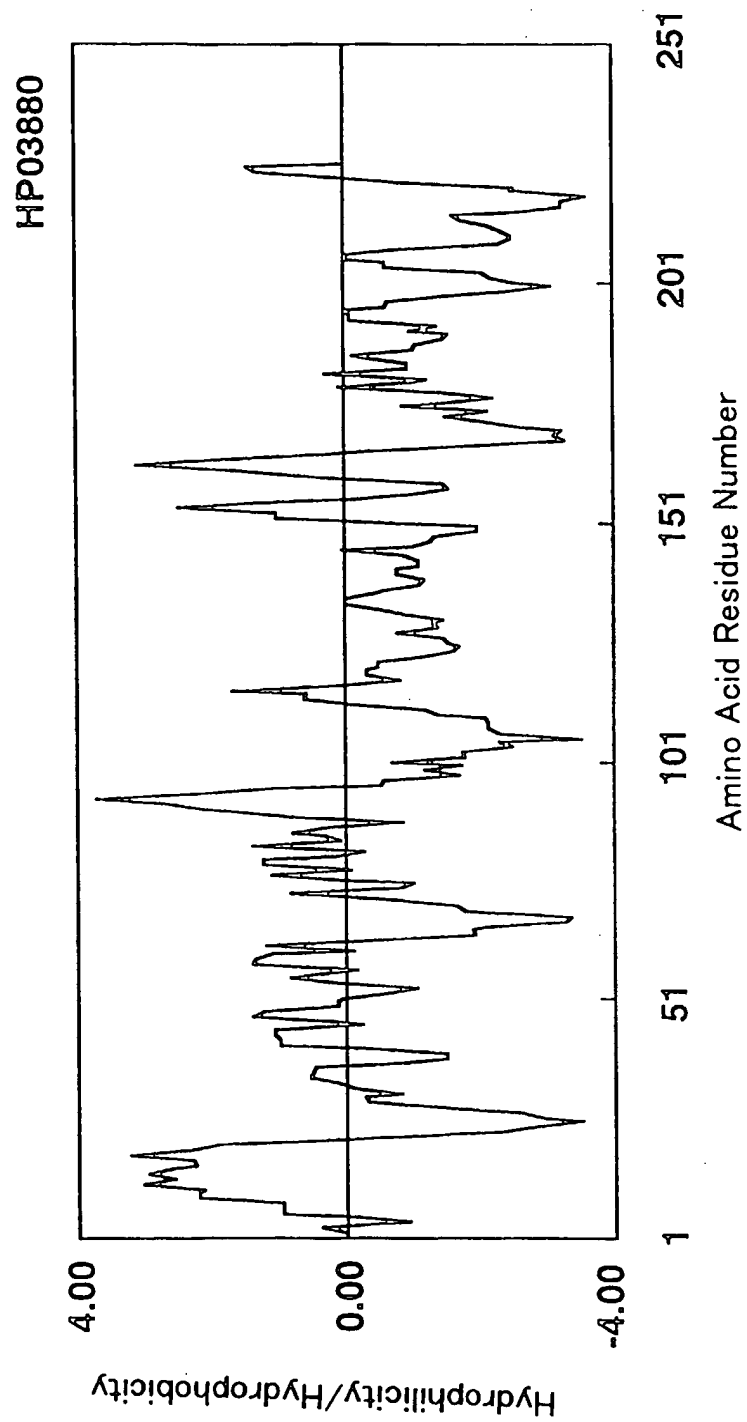
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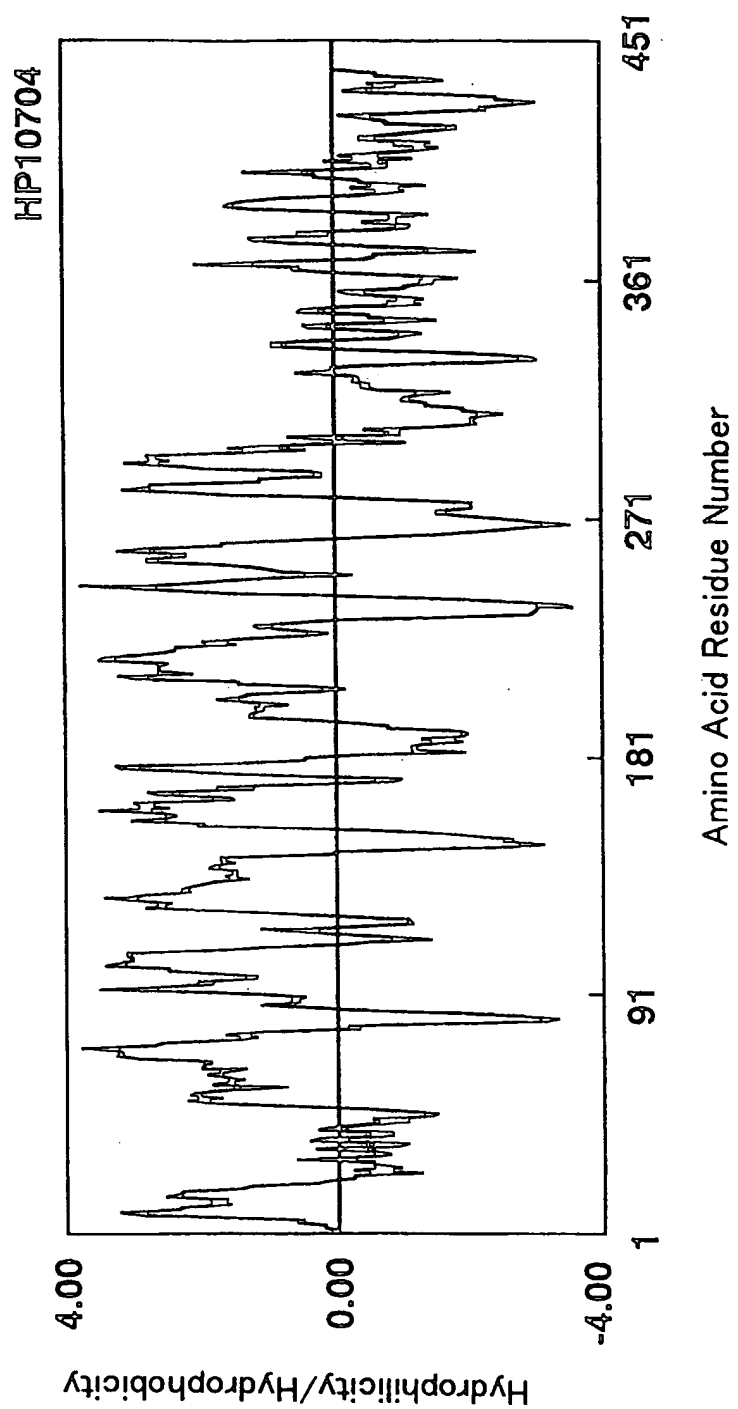
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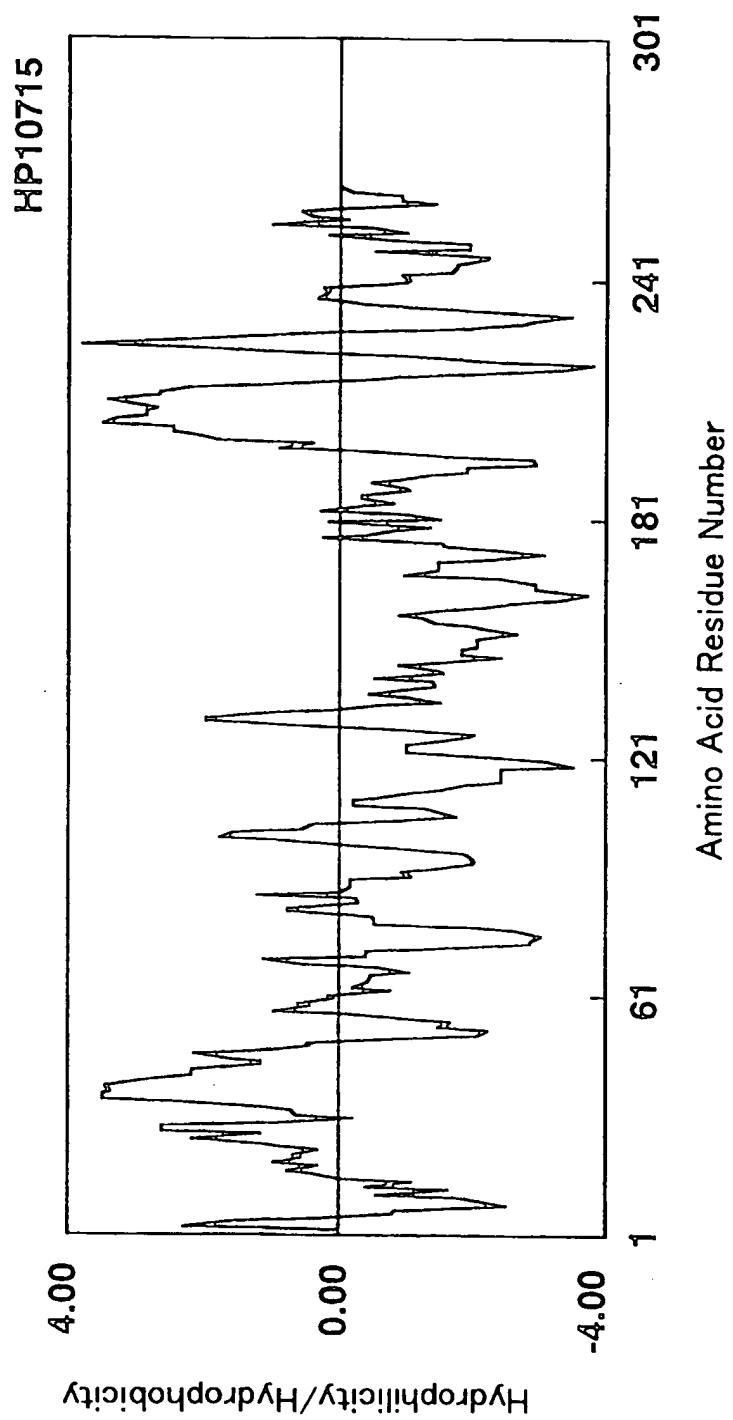
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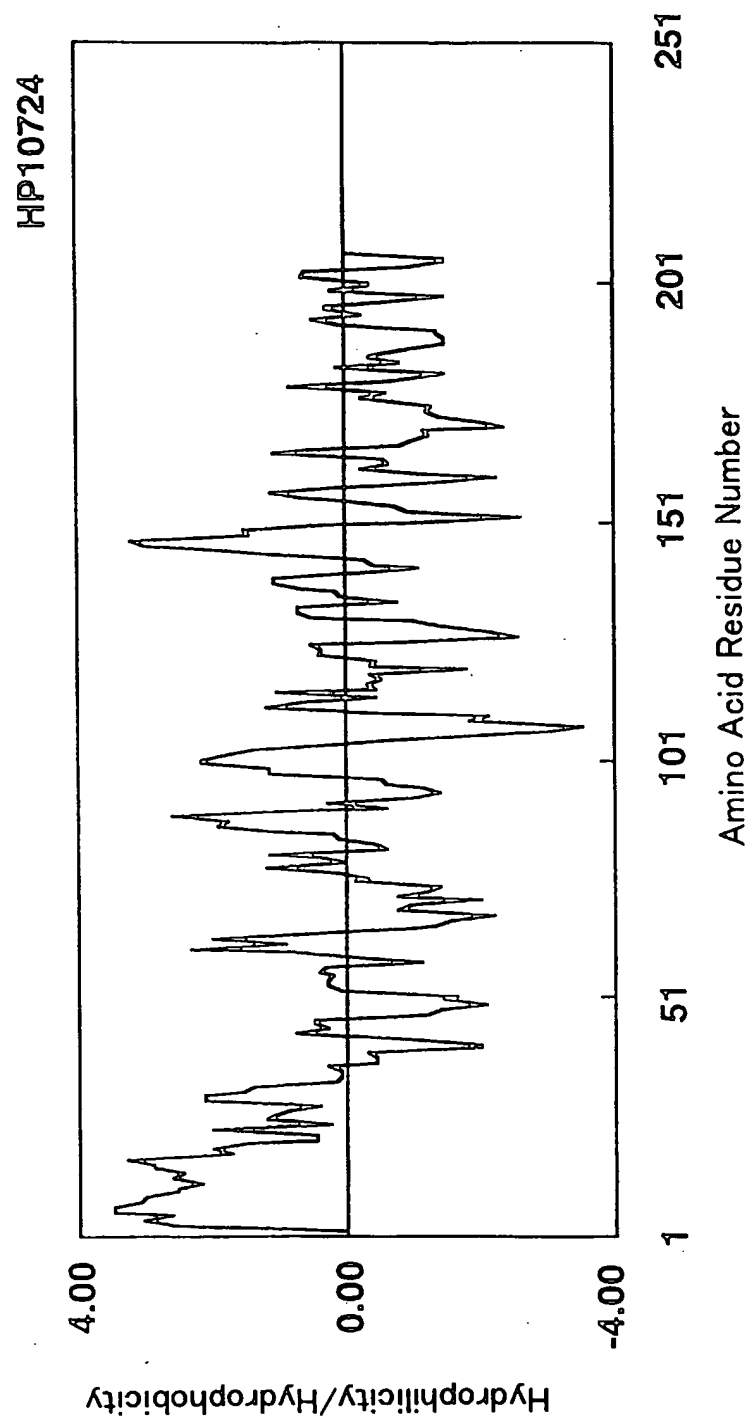
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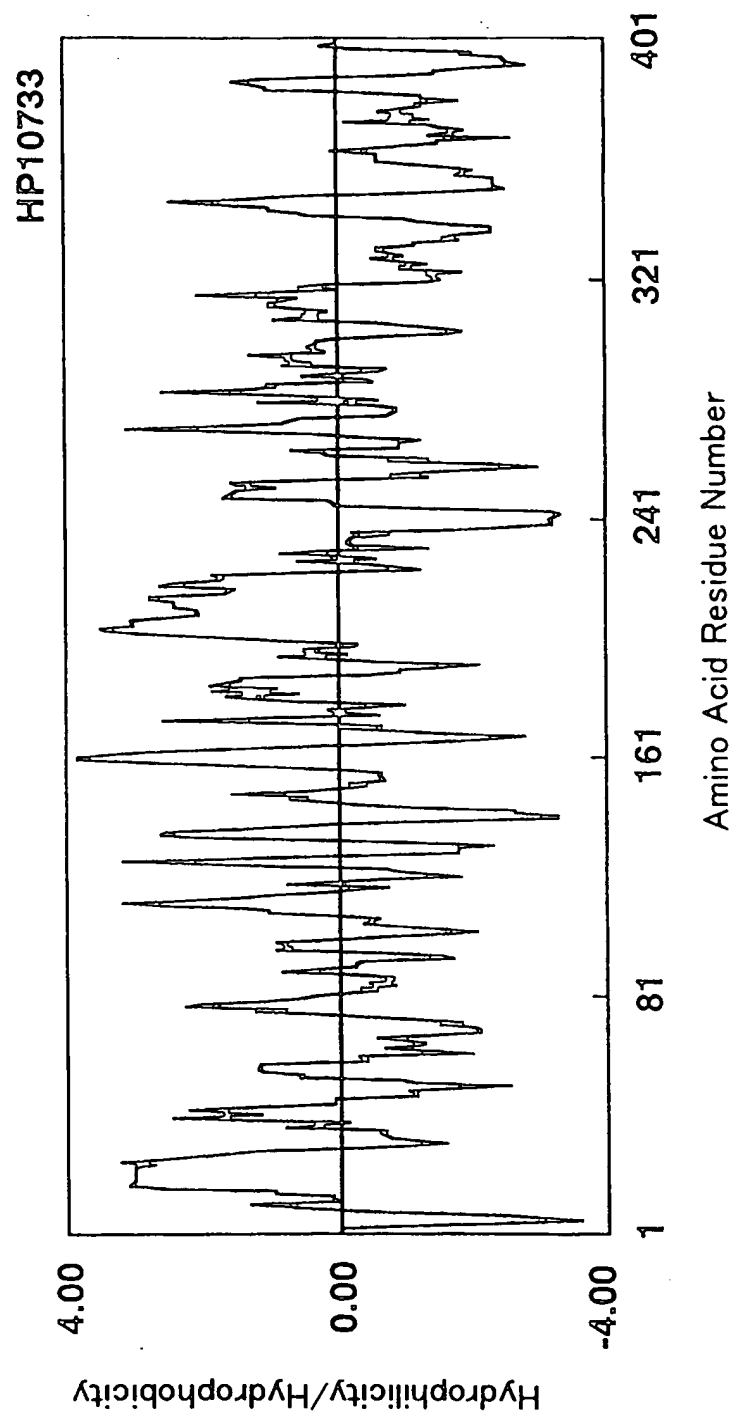
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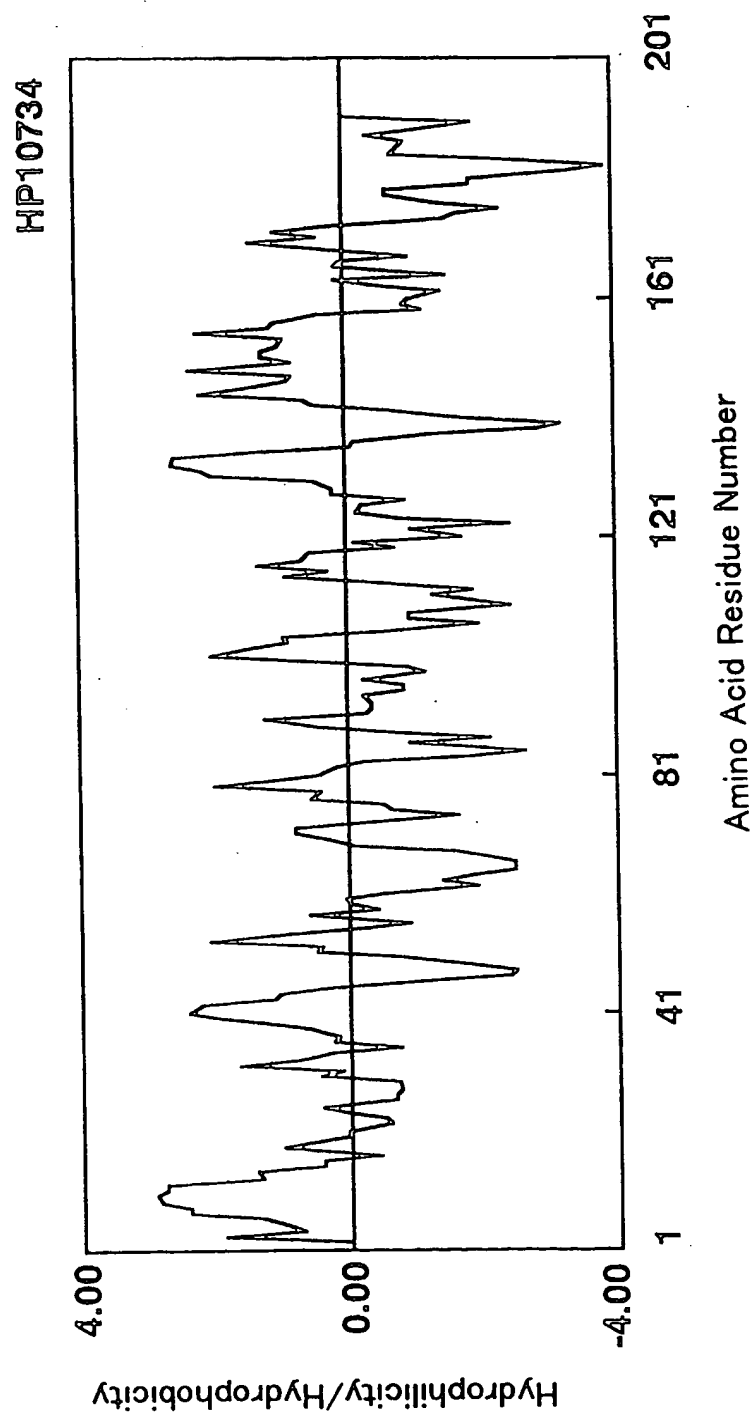
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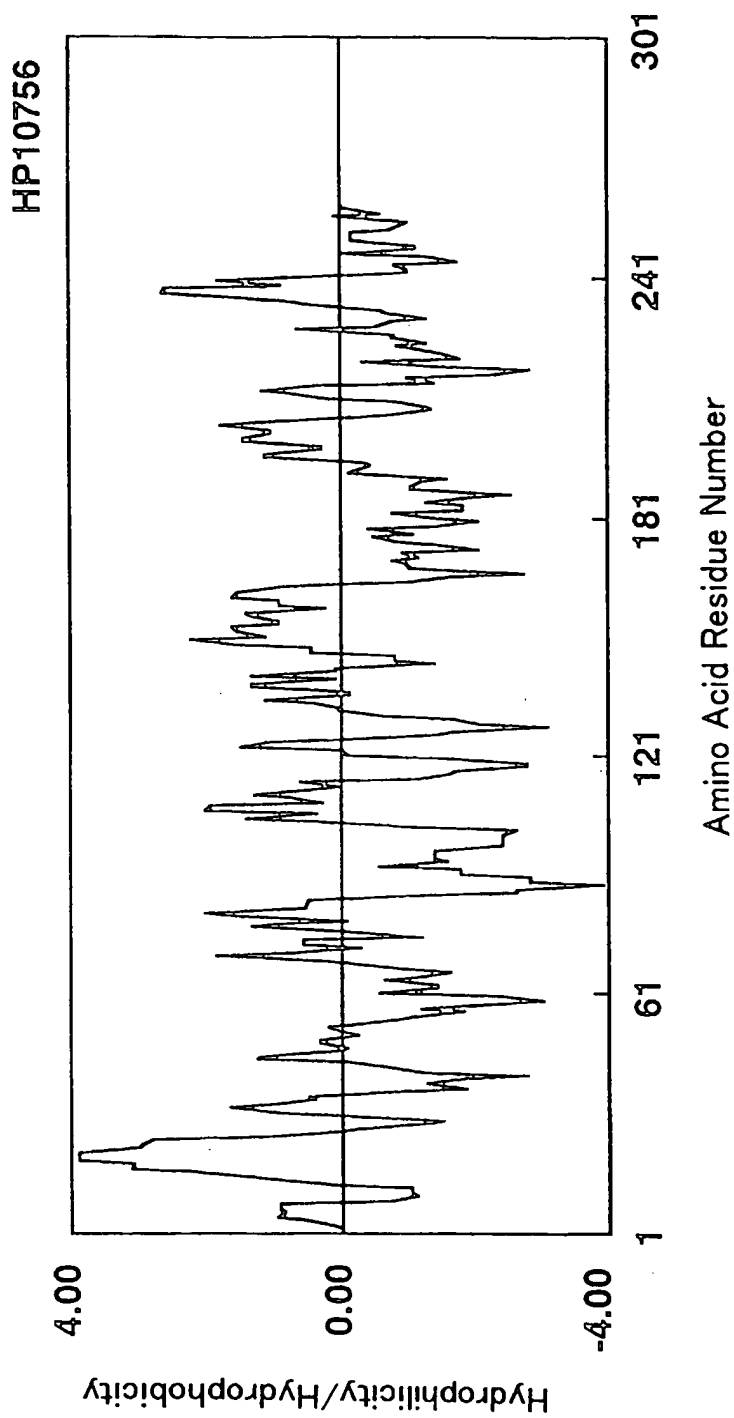
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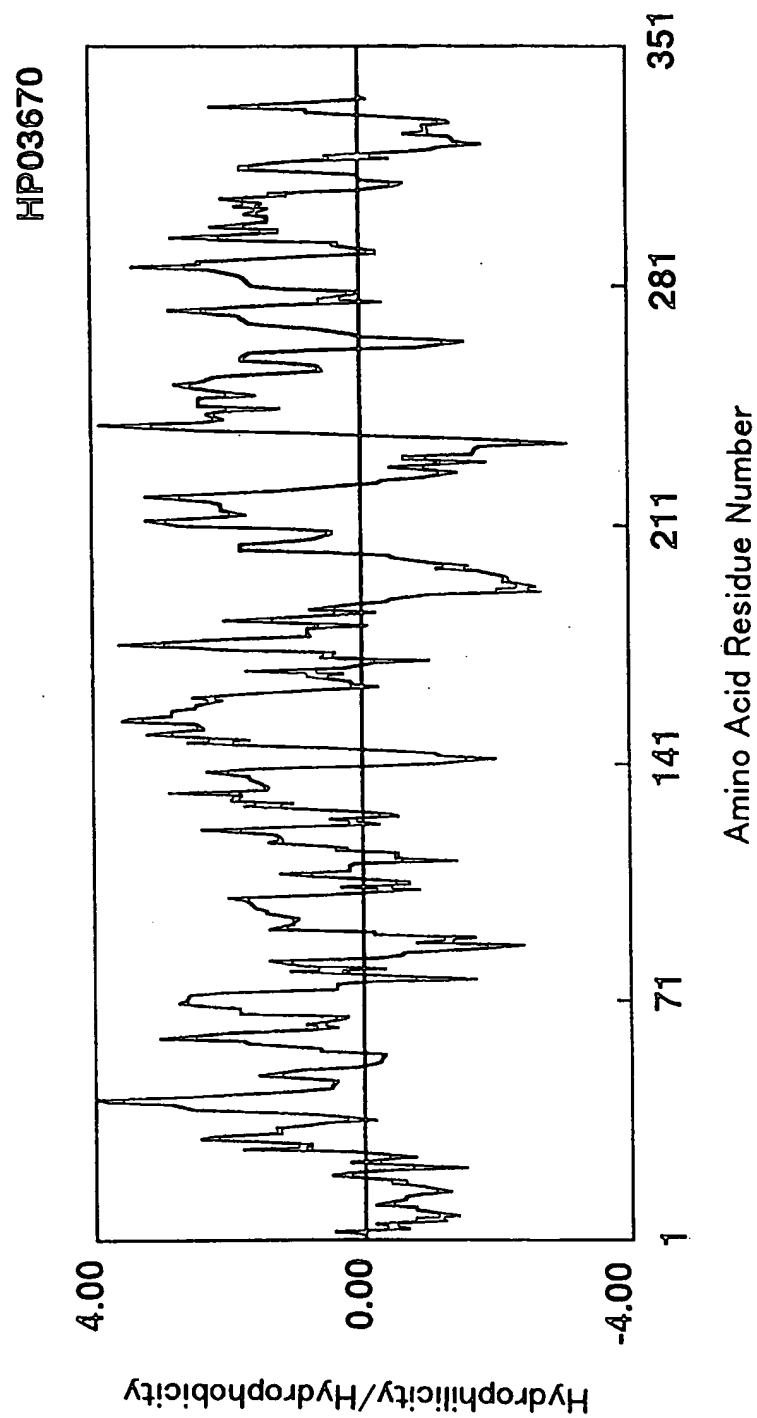
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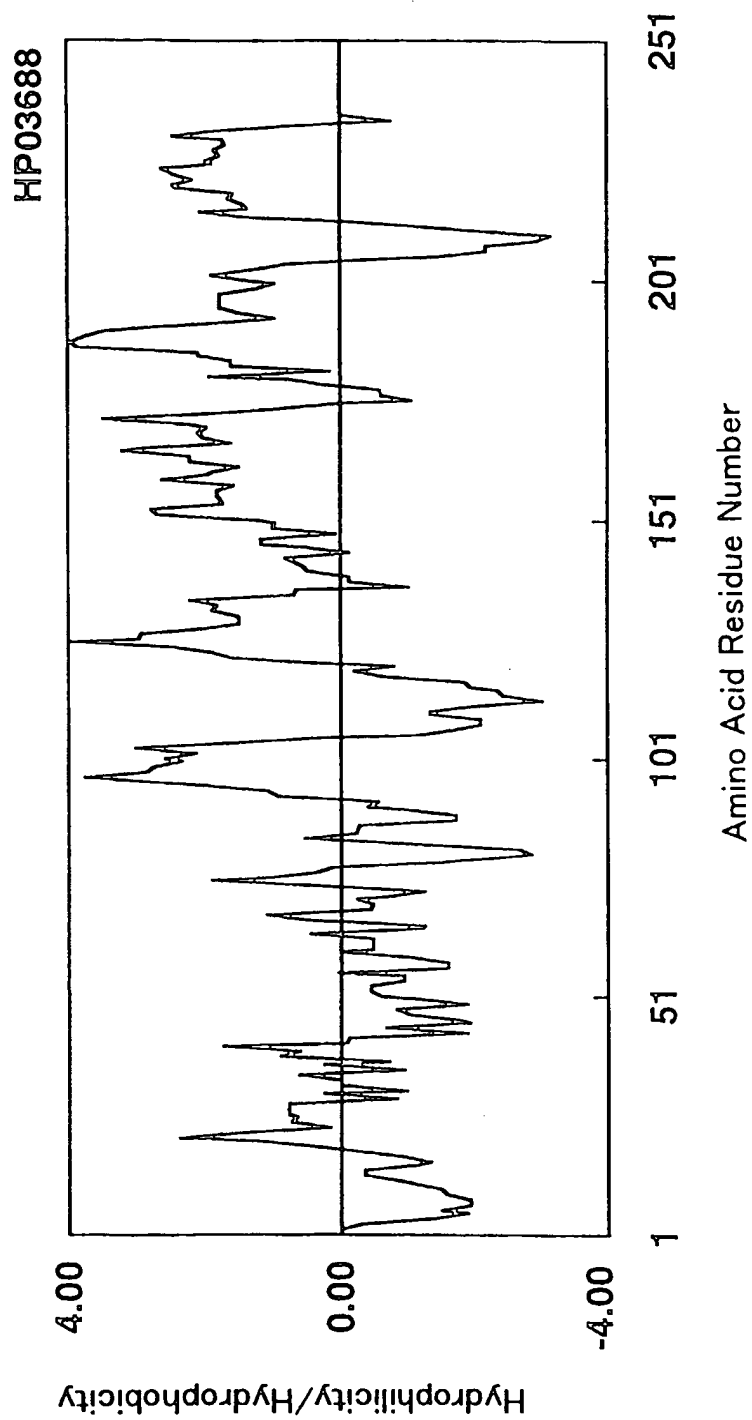
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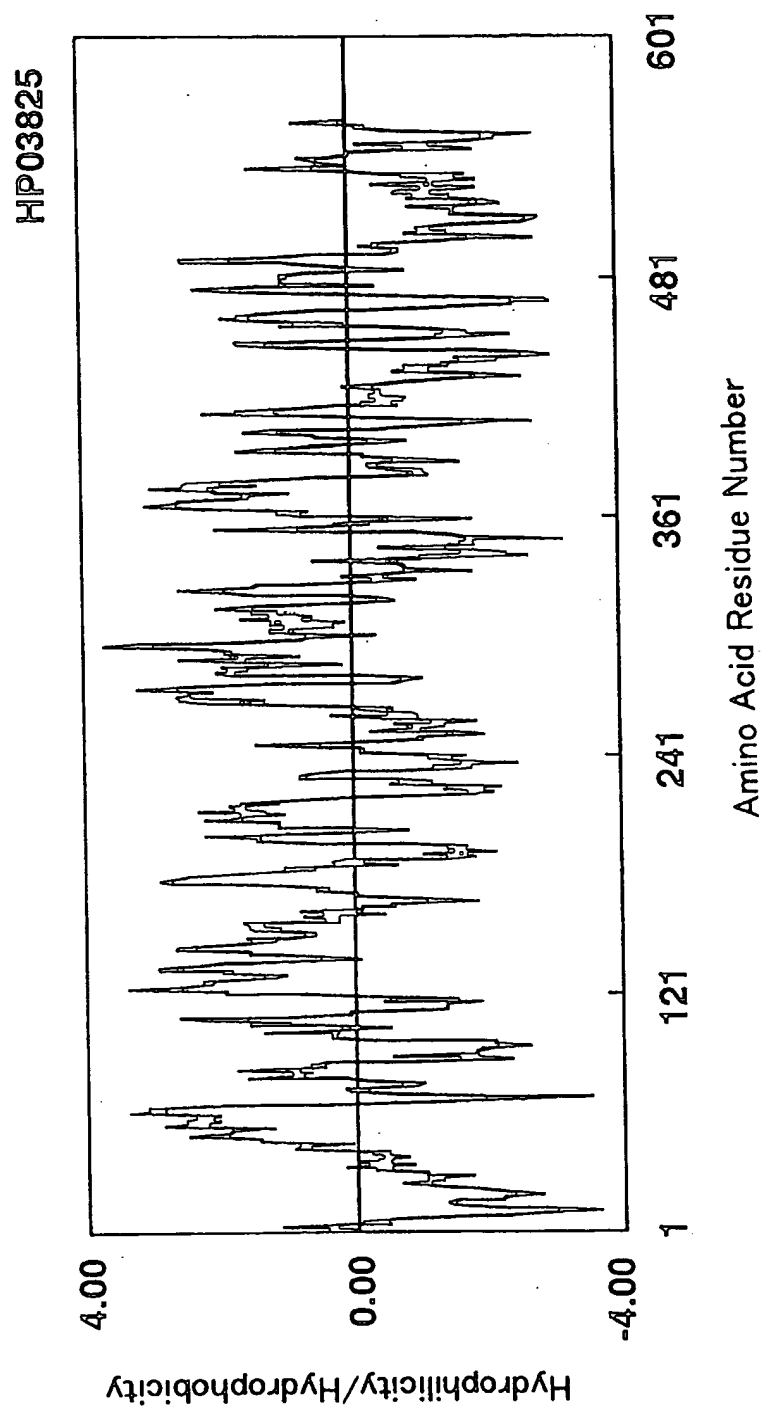
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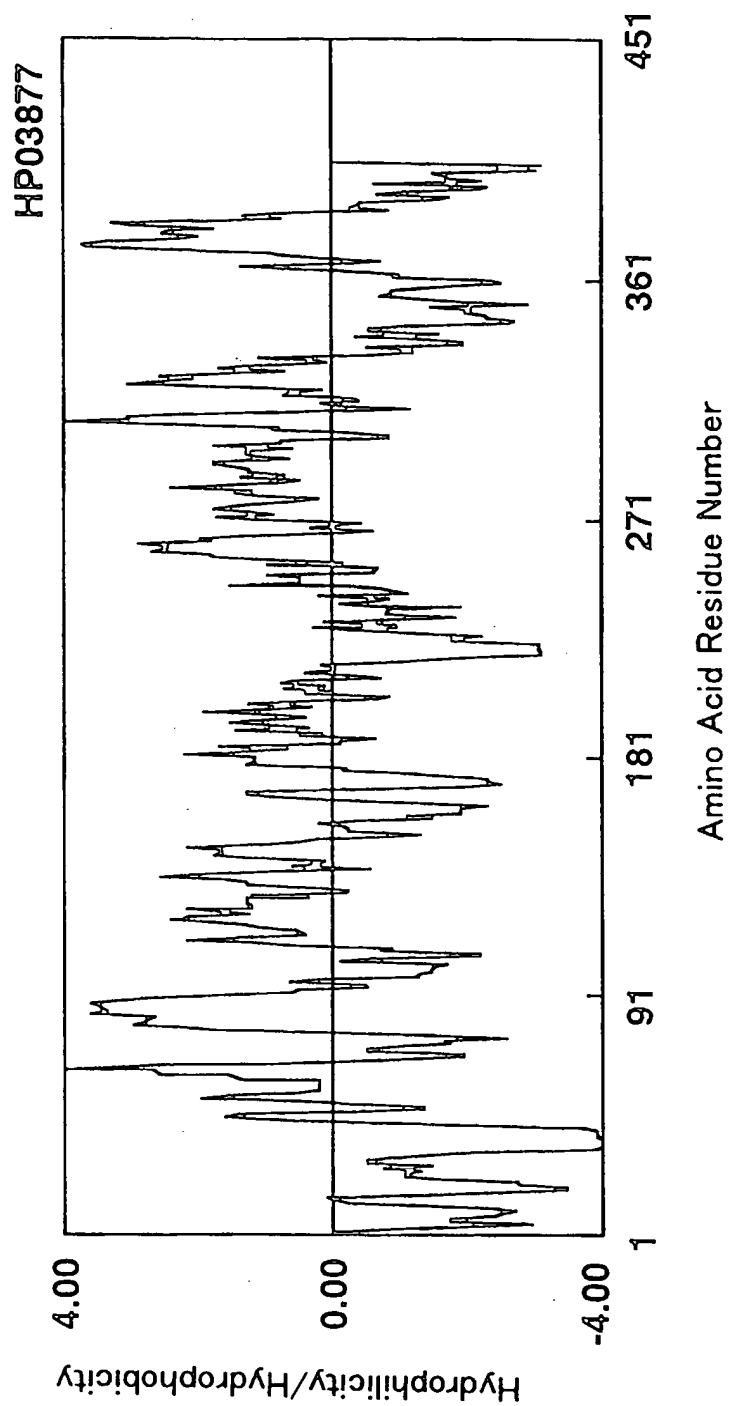
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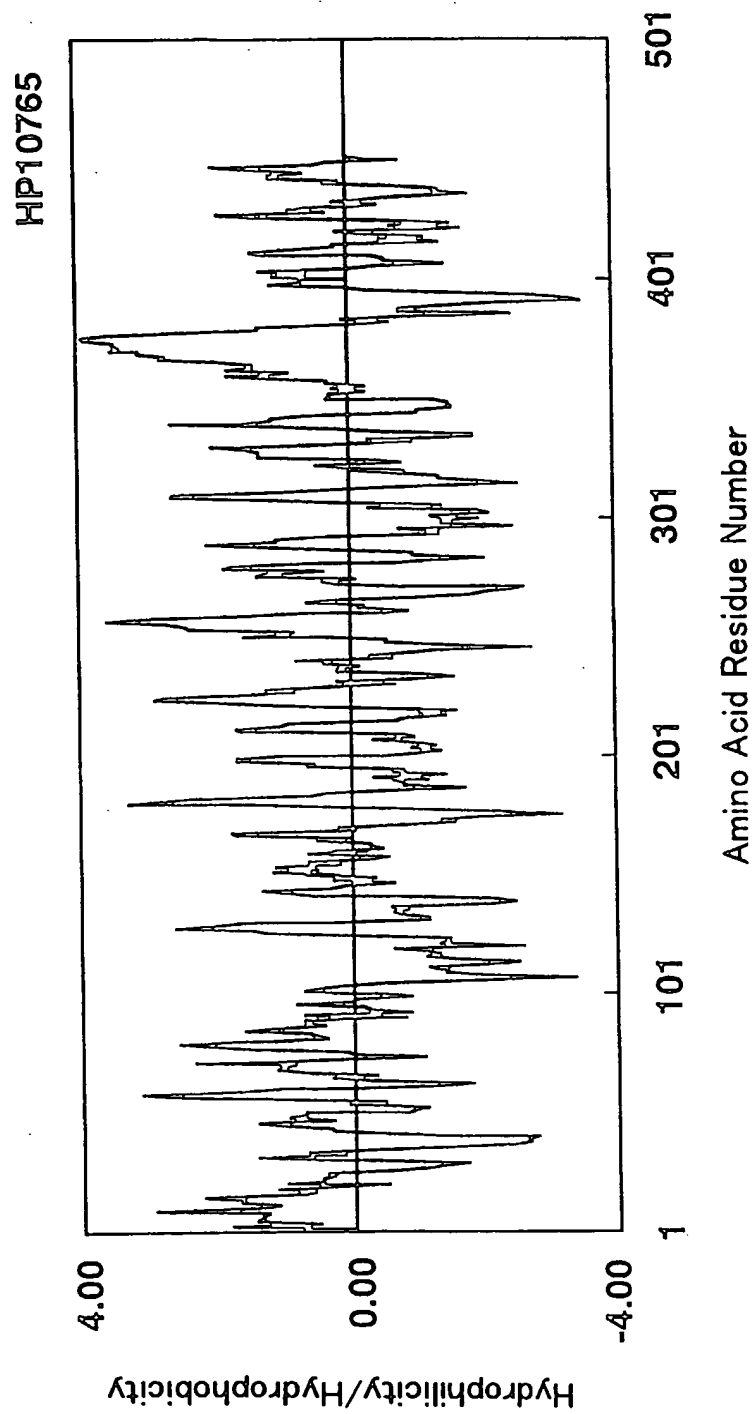
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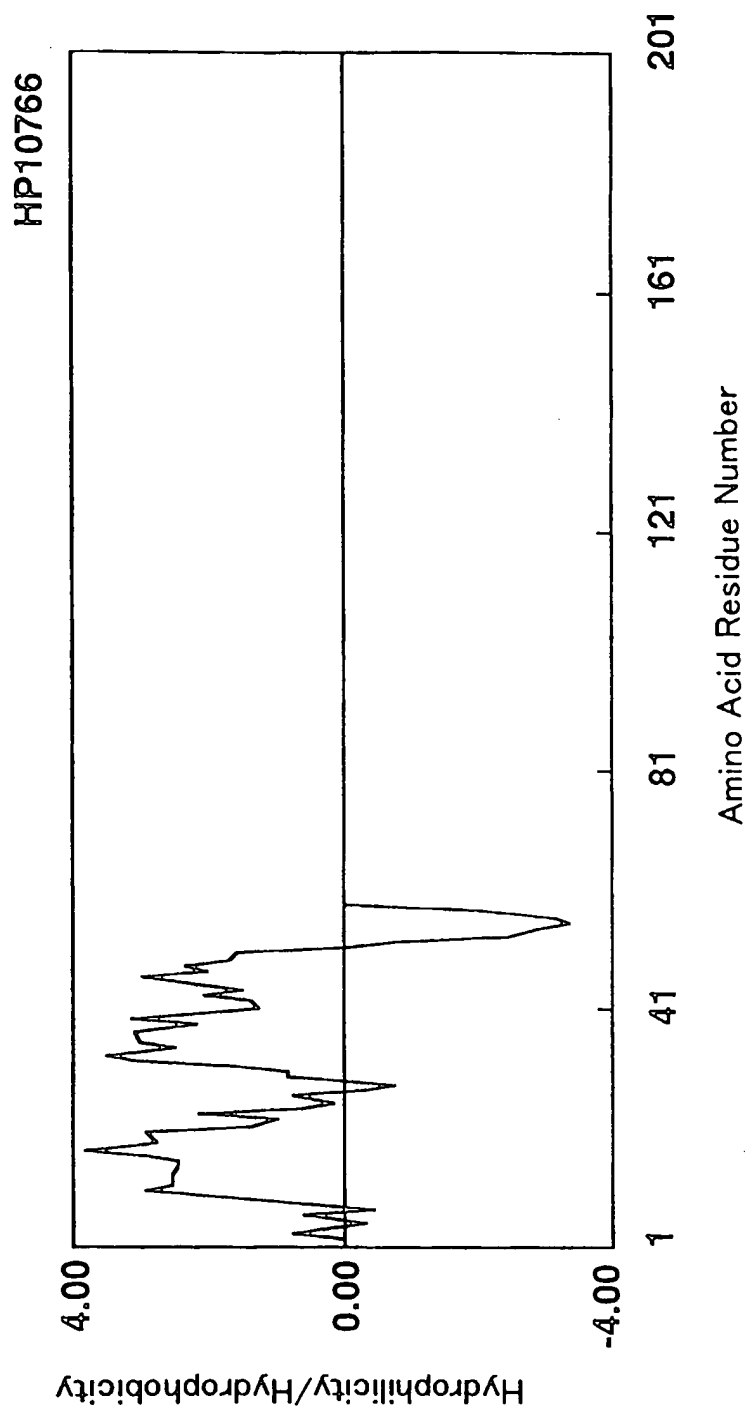
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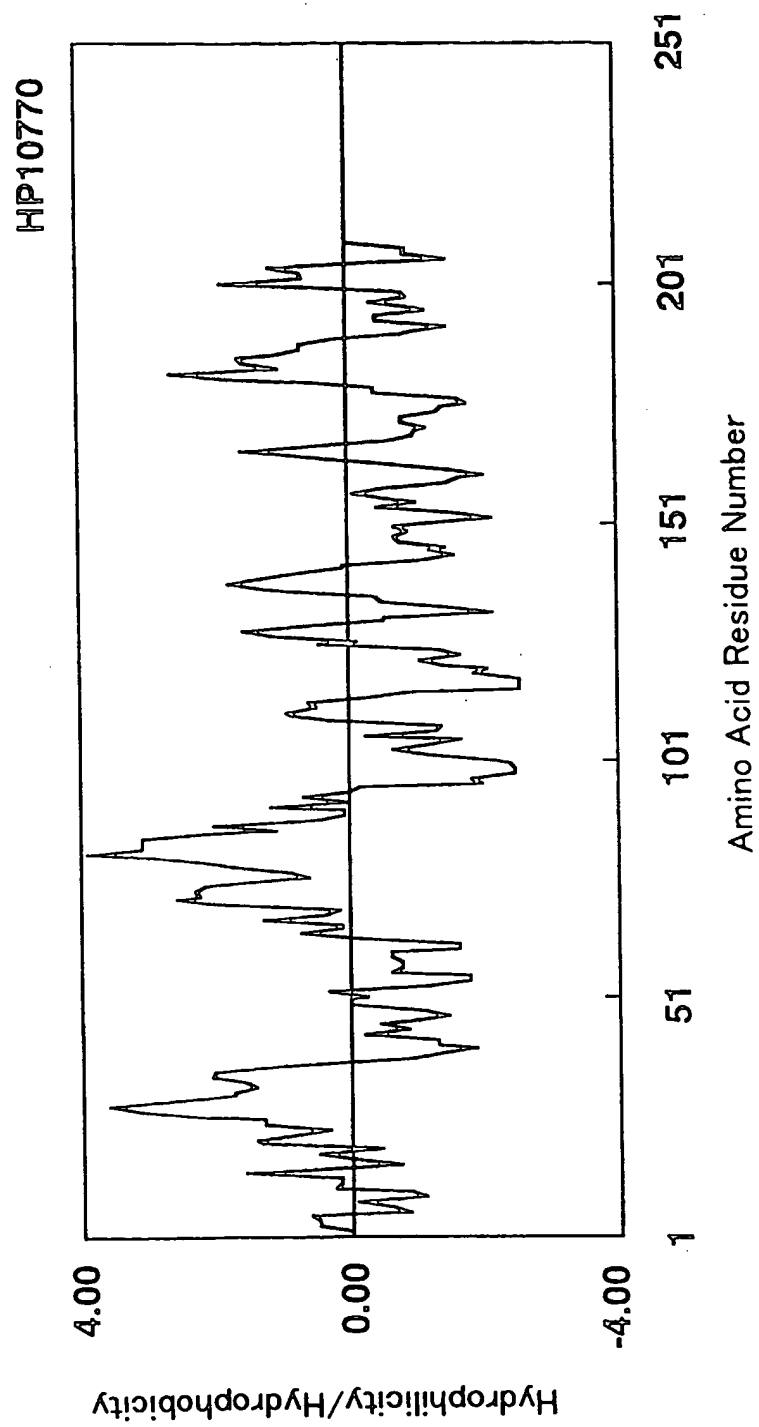
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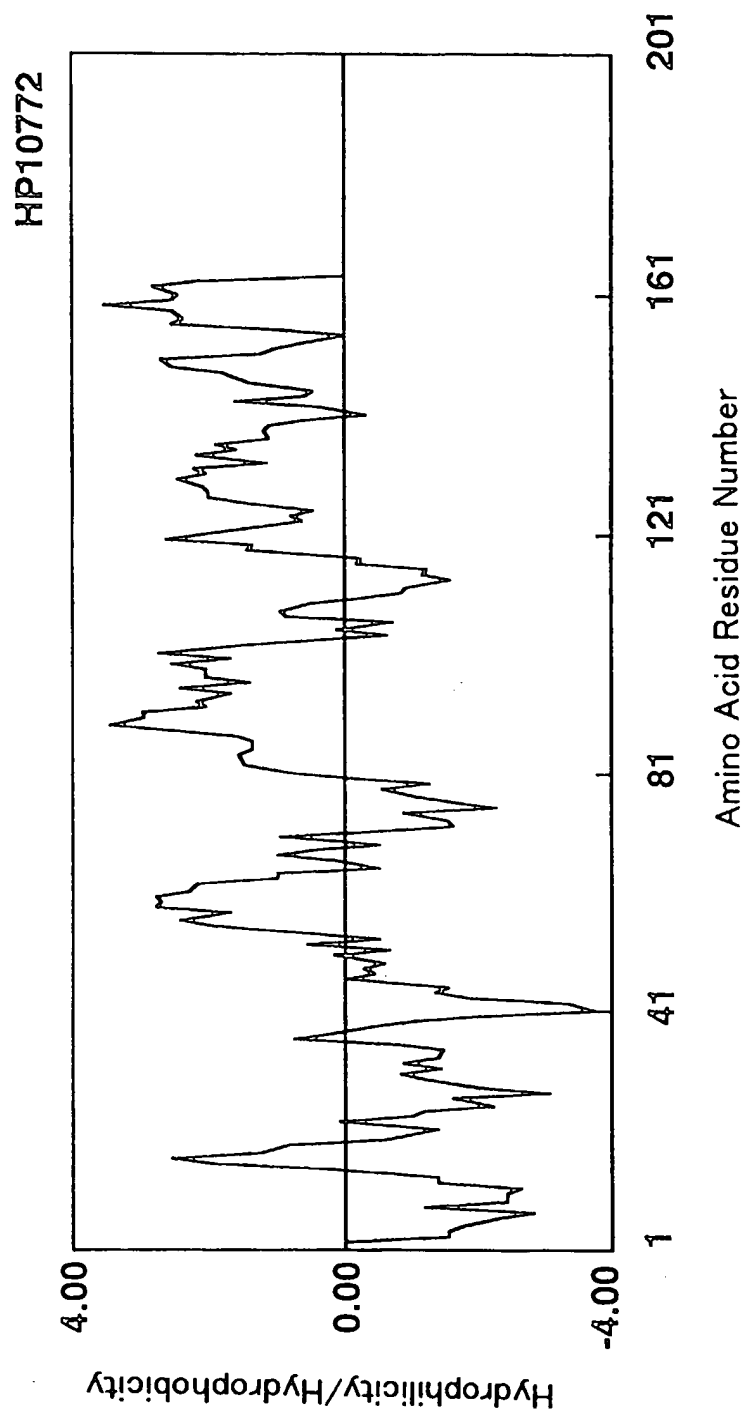
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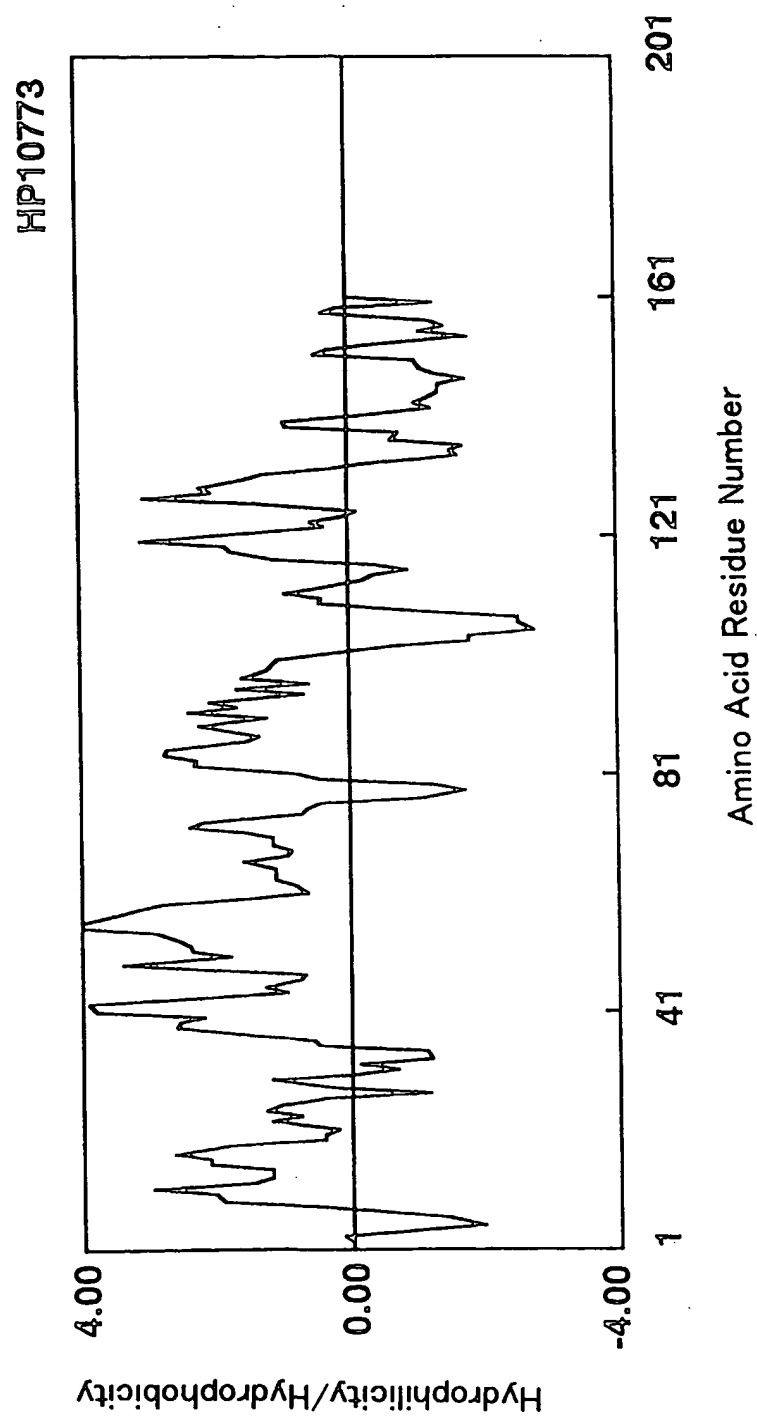
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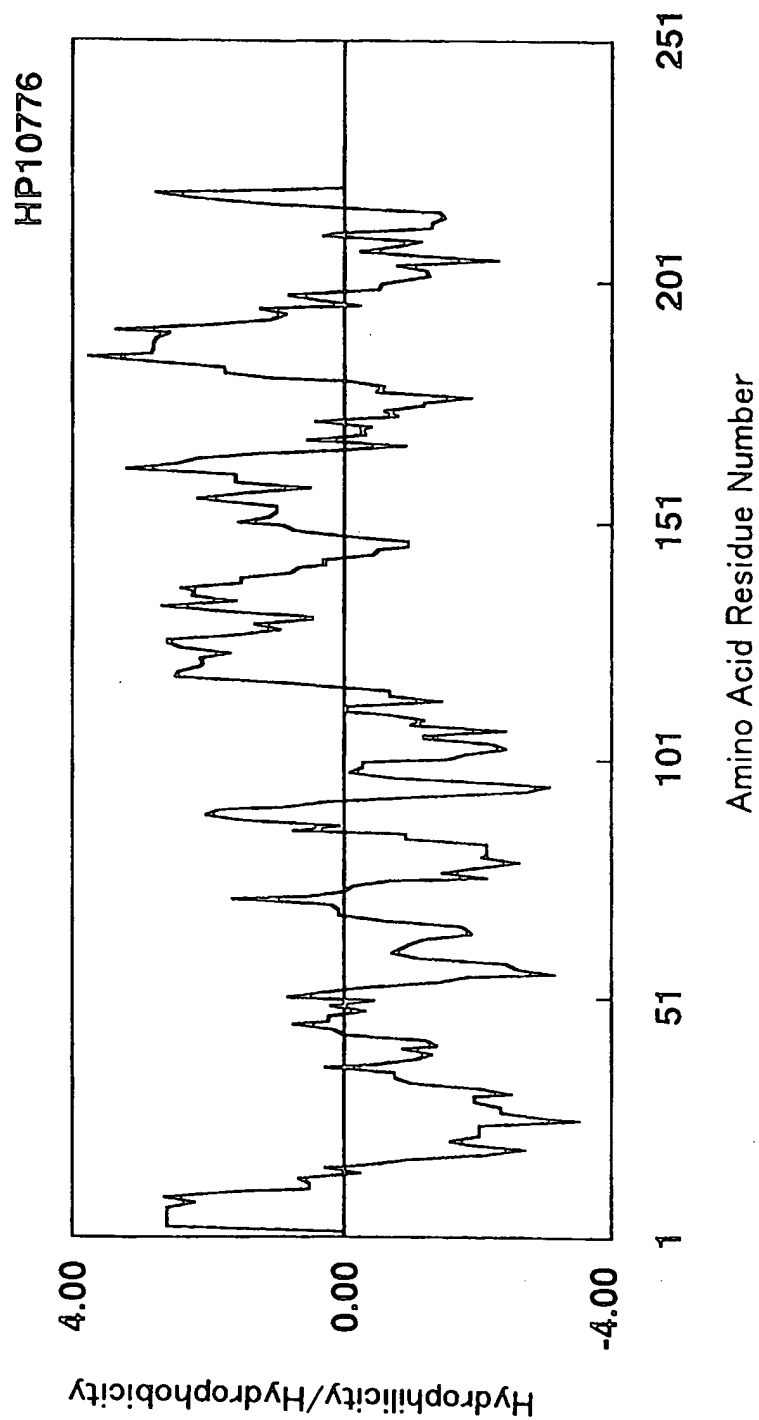
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4 /307

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Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg Gly Asn
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225                  230                  235                  240
Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
                  245                  250                  255
Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
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Tyr Ala Lys Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Leu

         35   40   45

Phe Leu Ile Val Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu

         50   55   60

Ala Ala Leu Leu Asn Ile Lys Glu Lys Thr Arg Leu Arg Ala Pro Pro

65   70   75   80

Asn Ala Thr Leu Glu His Phe Tyr Leu Thr Ser Gly Lys Gln Pro Lys

```
                 85                    90                    95
Gln Val Glu Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg
                100                   105                   110
Gln Val Glu Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser
            115                   120                   125
Leu Leu Lys Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu
            130                   135                   140
Ile Ala Phe Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe
145                   150                   155                   160
Tyr Asp Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile
                165                   170                   175
Pro Ser Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser
                180                   185                   190
Leu Leu Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu
            195                   200                   205
Gln Ile Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp
        210                   215                   220
Phe Ala Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp
225                   230                   235                   240
Ser Ser Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly
                245                   250                   255
Trp Lys Asn Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe
                260                   265                   270
Ile Ile Thr Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr
            275                   280                   285
```

Leu Val Tyr Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe
        290   295   300

Phe Asn Ser Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala
305   310   315   320

Tyr Leu Ile Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val
                325   330   335

Glu Asp Glu Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu
                340   345   350

Glu Ala Ala Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly
                355   360   365

His Pro Ile Leu Asn Asn Asn His Arg Lys Asn Asp
        370   375   380

<210> 5

<211> 585

<212> PRT

<213> Homo sapiens

<400> 5

Met Val Cys Arg Glu Gln Leu Ser Lys Asn Gln Val Lys Trp Val Phe
  1   5   10   15

Ala Gly Ile Thr Cys Val Ser Val Val Ile Ala Ala Ile Val Leu
                20   25   30

Ala Ile Thr Leu Arg Arg Pro Gly Cys Glu Leu Glu Ala Cys Ser Pro
        35   40   45

Asp Ala Asp Met Leu Asp Tyr Leu Leu Ser Leu Gly Gln Ile Ser Arg

```
        50                  55                  60
Arg Asp Ala Leu Glu Val Thr Trp Tyr His Ala Ala Asn Ser Lys Lys
  65              70                  75                  80
Ala Met Thr Ala Ala Leu Asn Ser Asn Ile Thr Val Leu Glu Ala Asp
              85                  90                  95
Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr Gly Val Pro Ile
              100                 105                 110
Met Ala His Pro Pro Thr Ile Tyr Ser Asp Asn Thr Leu Glu Gln Trp
              115                 120                 125
Leu Asp Ala Val Leu Gly Ser Ser Gln Lys Gly Ile Lys Leu Asp Phe
              130                 135                 140
Lys Asn Ile Lys Ala Val Gly Pro Ser Leu Asp Leu Leu Arg Gln Leu
  145              150                 155                 160
Thr Glu Glu Gly Lys Val Arg Arg Pro Ile Trp Ile Asn Ala Asp Ile
              165                 170                 175
Leu Lys Gly Pro Asn Met Leu Ile Ser Thr Glu Val Asn Ala Thr Gln
              180                 185                 190
Phe Leu Ala Leu Val Gln Glu Lys Tyr Pro Lys Ala Thr Leu Ser Pro
              195                 200                 205
Gly Trp Thr Thr Phe Tyr Met Ser Thr Ser Pro Asn Arg Thr Tyr Thr
              210                 215                 220
Gln Ala Met Val Glu Lys Met His Glu Leu Val Gly Gly Val Pro Gln
  225              230                 235                 240
Arg Val Thr Phe Pro Val Arg Ser Ser Met Val Arg Ala Ala Trp Pro
              245                 250                 255
```

His Phe Ser Trp Leu Leu Ser Gln Ser Glu Arg Tyr Ser Leu Thr Leu
           260   265   270

Trp Gln Ala Ala Ser Asp Pro Met Ser Val Glu Asp Leu Leu Tyr Val
         275   280   285

Arg Asp Asn Thr Ala Val His Gln Val Tyr Tyr Asp Ile Phe Glu Pro
  290   295   300

Leu Leu Ser Gln Phe Lys Gln Leu Ala Leu Asn Ala Thr Arg Lys Pro
305   310   315   320

Met Tyr Tyr Thr Gly Gly Ser Leu Ile Pro Leu Leu Gln Leu Pro Gly
         325   330   335

Asp Asp Gly Leu Asn Val Glu Trp Leu Val Pro Asp Val Gln Gly Ser
         340   345   350

Gly Lys Thr Ala Thr Met Thr Leu Pro Asp Thr Glu Gly Met Ile Leu
         355   360   365

Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro Val Pro Ile
  370   375   380

Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser Cys Leu Gln
385   390   395   400

Gln Leu Ala Thr His Pro Gly His Trp Gly Ile His Leu Gln Ile Ala
         405   410   415

Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala Arg Leu Ser
         420   425   430

Ser Leu Gly Leu Leu His Trp Pro Val Trp Val Gly Ala Lys Ile Ser
         435   440   445

His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg Glu Leu Leu

                450   455   460

Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala Pro Gly Trp

465   470   475   480

Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu Leu Thr Asp

                        485   490   495

Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser Phe Gln Met

                500   505   510

Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile Gly Arg Leu

                515   520   525

Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His Asn Pro Ala

        530   535   540

Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala Ala Arg Ala

545   550   555   560

Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly Tyr His Lys

                565   570   575

Asp Leu Leu Ala His Val Gly Arg Asn

        580   585

<210> 6

<211> 331

<212> PRT

<213> Homo sapiens

<400> 6

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe

    1   5   10   15

Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
　　　　　　　　　　20　　　　　　　　　　　　25　　　　　　　　　　　30

Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
　　　　　　　　35　　　　　　　　　　　40　　　　　　　　　　　45

Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
　　　　　50　　　　　　　　　　　55　　　　　　　　　　60

Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
65　　　　　　　　　　70　　　　　　　　　　75　　　　　　　　　　80

Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
　　　　　　　　　85　　　　　　　　　　90　　　　　　　　　　95

Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
　　　　　　　　100　　　　　　　　　105　　　　　　　　　110

Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp
　　　　　　　115　　　　　　　　　120　　　　　　　　　125

Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg
　　　　　130　　　　　　　　　135　　　　　　　　　140

Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala
145　　　　　　　　　150　　　　　　　　　155　　　　　　　　　160

Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys
　　　　　　　　165　　　　　　　　　170　　　　　　　　　175

Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu
　　　　　　　180　　　　　　　　　185　　　　　　　　　190

Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu
　　　　　195　　　　　　　　　200　　　　　　　　　205

Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu

```
            210                 215                 220
Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
    225                 230                 235                 240
Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
                    245                 250                 255
Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
                    260                 265                 270
Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
                275                 280                 285
Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
        290                 295                 300
Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr
305                 310                 315                 320
Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
                    325                 330
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<210> 7

<211> 345

<212> PRT

<213> Homo sapiens

<400> 7

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Met Ser Pro Glu Glu Trp Thr Tyr Leu Val Val Leu Leu Ile Ser Ile
    1                   5                   10                  15
Pro Ile Gly Phe Leu Phe Lys Lys Ala Gly Pro Gly Leu Lys Arg Trp
            20                  25                  30
```

Gly Ala Ala Ala Val Gly Leu Gly Leu Thr Leu Phe Thr Cys Gly Pro
          35   40   45

His Thr Leu His Ser Leu Val Thr Ile Leu Gly Thr Trp Ala Leu Ile
          50   55   60

Gln Ala Gln Pro Cys Ser Cys His Ala Leu Ala Leu Ala Trp Thr Phe
65   70   75   80

Ser Tyr Leu Leu Phe Phe Arg Ala Leu Ser Leu Leu Gly Leu Pro Thr
                  85   90   95

Pro Thr Pro Phe Thr Asn Ala Val Gln Leu Leu Leu Thr Leu Lys Leu
                  100   105   110

Val Ser Leu Ala Ser Glu Val Gln Asp Leu His Leu Ala Gln Arg Lys
              115   120   125

Glu Met Ala Ser Gly Phe Ser Lys Gly Pro Thr Leu Gly Leu Leu Pro
      130   135   140

Asp Val Pro Ser Leu Met Glu Thr Leu Ser Tyr Ser Tyr Cys Tyr Val
145   150   155   160

Gly Ile Met Thr Gly Pro Phe Phe Arg Tyr Arg Thr Tyr Leu Asp Trp
                  165   170   175

Leu Glu Gln Pro Phe Pro Gly Ala Val Pro Ser Leu Arg Pro Leu Leu
              180   185   190

Arg Arg Ala Trp Pro Ala Pro Leu Phe Gly Leu Leu Phe Leu Leu Ser
          195   200   205

Ser His Leu Phe Pro Leu Glu Ala Val Arg Glu Asp Ala Phe Tyr Ala
      210   215   220

Arg Pro Leu Pro Ala Arg Leu Phe Tyr Met Ile Pro Val Phe Phe Ala

225   230   235   240

Phe Arg Met Arg Phe Tyr Val Ala Trp Ile Ala Ala Glu Cys Gly Cys

                    245   250   255

Ile Ala Ala Gly Phe Gly Ala Tyr Pro Val Ala Ala Lys Ala Arg Ala

            260   265   270

Gly Gly Gly Pro Thr Leu Gln Cys Pro Pro Pro Ser Ser Pro Glu Lys

            275   280   285

Ala Ala Ser Leu Glu Tyr Asp Tyr Glu Thr Ile Arg Asn Ile Asp Cys

        290   295   300

Tyr Ser Thr Asp Phe Cys Val Arg Val Arg Asp Gly Met Arg Tyr Trp

305   310   315   320

Asn Met Thr Val Gln Trp Trp Leu Ala Gln Tyr Ile Tyr Lys Ser Ala

                325   330   335

Pro Ala Arg Ser Tyr Val Leu Arg Leu

            340   345

<210> 8

<211> 89

<212> PRT

<213> Homo sapiens

<400> 8

Met Tyr Met Gln Asp Tyr Trp Arg Thr Trp Leu Lys Gly Leu Arg Gly

    1   5   10   15

Phe Phe Phe Val Gly Val Leu Phe Ser Ala Val Ser Ile Ala Ala Phe

            20   25   30

Cys Thr Phe Leu Val Leu Ala Ile Thr Arg His Gln Ser Leu Thr Asp

     35   40   45

Pro Thr Ser Tyr Tyr Leu Ser Ser Val Trp Ser Phe Ile Ser Phe Lys

     50   55   60

Trp Ala Phe Leu Leu Ser Leu Tyr Ala His Arg Tyr Arg Ala Asp Phe

65   70   75   80

Ala Asp Ile Ser Ile Leu Ser Asp Phe

     85

<210> 9

<211> 406

<212> PRT

<213> Homo sapiens

<400> 9

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro

 1   5   10   15

Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly

     20   25   30

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn

     35   40   45

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

     50   55   60

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val

65   70   75   80

Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp

                    85   90   95

Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro

                   100   105   110

Lys Asp Ser Ile Gln Phe Ser Ser Ala Leu Val Phe Thr Arg Leu Leu

             115   120   125

Glu Phe Asp Ser Thr Asn Val Ser Asp Thr Ala Ala Lys Pro Leu Gly

           130   135   140

Arg Pro Tyr Pro Pro Tyr Ser Leu Ala Asp Phe Ser Trp Asn Asn Ile

145   150   155   160

Thr Asp Ser Leu Asp Pro Ala Thr Leu Ser Ala Thr Phe Gln Gly His

                   165   170   175

Pro Met Asn Asp Pro Thr Arg Thr Phe Ala Asn Gly Ser Leu Ala Phe

                   180   185   190

Arg Val Gln Ala Phe Ser Arg Ser Ser Arg Pro Ala Gln Pro Pro Arg

             195   200   205

Leu Leu His Thr Ala Asp Thr Cys Gln Leu Glu Val Ala Leu Ile Gly

           210   215   220

Ala Ser Pro Arg Gly Asn Arg Ser Leu Phe Gly Leu Glu Val Ala Thr

225   230   235   240

Leu Gly Gln Gly Pro Asp Cys Pro Ser Met Gln Glu Gln His Ser Ile

                   245   250   255

Asp Asp Glu Tyr Ala Pro Ala Val Phe Gln Leu Asp Gln Leu Leu Trp

             260   265   270

Gly Ser Leu Pro Ser Gly Phe Ala Gln Trp Arg Pro Val Ala Tyr Ser

           275   280   285

```
Gln Lys Pro Gly Gly Arg Glu Ser Ala Leu Pro Cys Gln Ala Ser Pro
    290             295             300

Leu His Pro Ala Leu Ala Tyr Ser Leu Pro Gln Ser Pro Ile Val Arg
305             310             315             320

Ala Phe Phe Gly Ser Gln Asn Asn Phe Cys Ala Phe Asn Leu Thr Phe
                325             330             335

Gly Ala Ser Thr Gly Pro Gly Tyr Trp Asp Gln His Tyr Leu Ser Trp
                340             345             350

Ser Met Leu Leu Gly Val Gly Phe Pro Pro Val Asp Gly Leu Ser Pro
                355             360             365

Leu Val Leu Gly Ile Met Ala Val Ala Leu Gly Ala Pro Gly Leu Met
    370             375             380

Leu Leu Gly Gly Gly Leu Val Leu Leu Leu His His Lys Lys Tyr Ser
385             390             395             400

Glu Tyr Gln Ser Ile Asn
                405
```

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<210> 10

<211> 192

<212> PRT

<213> Homo sapiens

<400> 10

Met Thr Ala Val Gly Val Gln Ala Gln Arg Pro Leu Gly Gln Arg Gln
  1             5               10              15

Pro Arg Arg Ser Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr
```

                    20   25   30

Cys Val Ala Leu Ala Val Val Leu Ser Ser Val Ser Ile Cys Asp Gly

                        35   40   45

His Trp Leu Leu Ala Glu Asp Arg Leu Phe Gly Leu Trp His Phe Cys

            50   55   60

Thr Thr Thr Asn Gln Ser Val Pro Ile Cys Phe Arg Asp Leu Gly Gln

        65   70   75   80

Ala His Val Pro Gly Leu Ala Val Gly Met Gly Leu Val Arg Ser Val

                    85   90   95

Gly Ala Leu Ala Val Val Ala Ala Ile Phe Gly Leu Glu Phe Leu Met

                    100   105   110

Val Ser Gln Leu Cys Glu Asp Lys His Ser Gln Cys Lys Trp Val Met

                    115   120   125

Gly Ser Ile Leu Leu Leu Val Ser Phe Val Leu Ser Ser Gly Gly Leu

            130   135   140

Leu Gly Phe Val Ile Leu Leu Arg Asn Gln Val Thr Leu Ile Gly Phe

        145   150   155   160

Thr Leu Met Phe Trp Cys Glu Phe Thr Ala Ser Phe Leu Leu Phe Leu

                    165   170   175

Asn Ala Ile Ser Gly Leu His Ile Asn Ser Ile Thr His Pro Trp Glu

                    180   185   190

<210> 11

<211> 801

<212> DNA

<213> Homo sapiens

<400> 11

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atggtgaaga ttagcttcca gcccgccgtg gctggcatca agggcgacaa ggctgacaag    60

gcgtcggcgt cggcccctgc gccggcctcg gccaccgaga tcctgctgac gccggctagg   120

gaggagcagc ccccacaaca tcgatccaag aggggggagct cagtgggcgg cgtgtgctac   180

ctgtcgatgg gcatggtcgt gctgctcatg ggcctcgtgt tcgcctctgt ctacatctac   240

agatacttct ttcttgcaca gctggcccga gataacttct tccgctgtgg tgtgctgtat   300

gaggactccc tgtcctccca ggtccggact cagatggagc tggaagagga tgtgaaaatc   360

tacctcgacg agaactacga gcgcatcaac gtgcctgtgc cccagtttgg cggcggtgac   420

cctgcagaca tcatccatga cttccagcgg ggtctgactg cgtaccatga tatctccctg   480

gacaagtgct atgtcatcga actcaacacc accattgtgc tgccccctcg caacttctgg   540

gagctcctca tgaacgtgaa gaggggggacc tacctgccgc agacgtacat catccaggag   600

gagatggtgg tcacggagca tgtcagtgac aaggaggccc tggggtcctt catctaccac   660

ctgtgcaacg ggaaagacac ctaccggctc cggcgccggg caacgcggag gcggatcaac   720

aagcgtgggg ccaagaactg caatgccatc cgccacttcg agaacacctt cgtggtggag   780

acgctcatct gcggggtggt g                                             801
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<210> 12

<211> 1257

<212> DNA

<213> Homo sapiens

<400> 12

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atgagctgcg cggggcgggc gggccctgcc cggctcgccg cgctcgccct gctgacctgc    60

agcctgtggc cggcacgggc agacaacgcg agccaggagt actacacggc gctcatcaac   120

gtgacggtgc aggagcccgg ccgcggcgcc ccgctcacgt ttcgcatcga ccgcgggcgc   180
```

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tacgggcttg actcccccaa ggccgaggtc cgcggccagg tgctggcgcc gctgcccctc      240

cacggagttg ctgatcatct gggctgtgat ccacaaaccc ggttctttgt ccctcctaat      300

atcaaacagt ggattgcctt gctgcagagg ggaaactgca cgtttaaaga gaaaatatca      360

cgggccgctt ccacaatgc agttgctgta gtcatctaca ataataaatc caaagaggag       420

ccagttacca tgactcatcc aggcactgga gatattattg ctgtcatgat aacagaattg      480

aggggtaagg atattttgag ttatctggag aaaaacatct ctgtacaaat gacaatagct      540

gttggaactc gaatgccacc gaagaacttc agccgtggct ctctagtctt cgtgtcaata      600

tcctttattg ttttgatgat tatttcttca gcatggctca tattctactt cattcagaag      660

atcaggtaca caaatgcacg cgacaggaac cagcgtcgtc tcggagatgc agccaagaaa      720

gccatcagta aattgacaac caggacagta aagaagggtg acaaggaaac tgacccagac      780

tttgatcatt gtgcagtctg catagagagc tataagcaga atgatgtcgt ccgaattctc      840

ccctgcaagc atgttttcca caaatcctgc gtggatccct ggcttagtga acattgtacc      900

tgtcctatgt gcaaacttaa tatattgaag gccctgggaa ttgtgccgaa tttgccatgt      960

actgataacg tagcattcga tatggaaagg ctcaccagaa cccaagctgt taaccgaaga     1020

tcagccctcg gcgacctcgc cggcgacaac tcccttggcc ttgagccact tcgaacttcg     1080

gggatctcac ctcttcctca ggatggggag ctcactccga gaacaggaga aatcaacatt     1140

gcagtaacaa aagaatggtt tattattgcc agttttggcc tcctcagtgc cctcacactc     1200

tgctacatga tcatcagagc cacagctagc ttgaatgcta atgaggtaga atggttt        1257
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<210> 13

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 13

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atgaggggcg cgaacgcctg ggcgccactc tgcctgctgc tggctgccgc cacccagctc       60
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tcgcggcagc agtccccaga gagacctgtt ttcacatgtg gtggcattct tactggagag    120

tctggattta ttggcagtga aggttttcct ggagtgtacc ctccaaatag caaatgtact    180

tggaaaatca cagttcccga aggaaaagta gtcgttctca atttccgatt catagacctc    240

gagagtgaca acctgtgccg ctatgacttt gtggatgtgt acaatggcca tgccaatggc    300

cagcgcattg gccgcttctg tggcactttc cggcctggag cccttgtgtc cagtggcaac    360

aagatgatgg tgcagatgat ttctgatgcc aacacagctg gcaatggctt catggccatg    420

ttctccgctg ctgaaccaaa cgaaagaggg gatcagtatt gtggaggact ccttgacaga    480

ccttccggct ctttttaaaac ccccaactgg ccagaccggg attaccctgc aggagtcact    540

tgtgtgtggc acattgtagc cccaaagaat cagcttatag aattaaagtt tgagaagttt    600

gatgtggagc gagataacta ctgccgatat gattatgtgg ctgtgtttaa tggcgggggaa   660

gtcaacgatg ctagaagaat tggaaagtat tgtggtgata gtccacctgc gccaattgtg    720

tctgagagaa atgaacttct tattcagttt ttatcagact taagtttaac tgcagatggg    780

tttattggtc actacatatt caggccaaaa aaactgccta caactacaga acagcctgtc    840

accaccacat tccctgtaac cacgggttta aaaaccaccg tggccttgtg tcaacaaaag    900

tgtagacgga cggggactct ggagggcaat tattgttcaa gtgactttgt attagccggc    960

actgttatca caaccatcac tcgcgatggg agtttgcacg ccacagtctc gatcatcaac    1020

atctacaaag agggaaattt ggcgattcag caggcgggca agaacatgag tgccaggctg    1080

actgtcgtct gcaagcagtg ccctctcctc agaagaggtc taaattacat tattatgggc    1140

caagtaggtg aagatgggcg aggcaaaatc atgccaaaca gctttatcat gatgttcaag    1200

accaagaatc agaagctcct ggatgcctta aaaaataagc aatgt                    1245
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<210> 14

<211> 1140

<212> DNA

<213> Homo sapiens

<400> 14

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atcacgctgc ccctggcctt gctcttcctc atcgttcgat acttctttga gctgtacgtg   180

gctacaccac tggctgccct cttgaacata aaggagaaaa ctcggctgcg ggcacctccc   240

aacgccacct tggaacattt ctacctgacc agtggcaagc agcccaagca ggtggaagta   300

gagcttttgt cccggcagag cgggctctct ggccgccagg tagagcgttg gttccgtcgc   360

cgccgcaacc aggaccggcc cagtctcctc aagaagttcc gagaagccag ctggagattc   420

acattttacc tgattgcctt cattgccggc atggccgtca ttgtggataa accctggttc   480

tatgacatga agaaagtttg ggagggatat cccatacaga gcactatccc ttcccagtat   540

tggtactaca tgattgaact ttccttctac tggtccctgc tcttcagcat tgcctctgat   600

gtcaagcgaa aggatttcaa ggaacagatc atccaccatg tggccaccat cattctcatc   660

agcttttcct ggtttgccaa ttacatccga gctgggactc taatcatggc tctgcatgac   720

tcttccgatt acctgctgga gtcagccaag atgtttaact acgcgggatg gaagaacacc   780

tgcaacaaca tcttcatcgt cttcgccatt gtttttatca tcacccgact ggtcatcctg   840

cccttctgga tcctgcattg caccctggtg tacccactgg agctctatcc tgccttcttt   900

ggctattact tcttcaattc catgatggga gttctacagc tgctgcatat cttctgggcc   960

tacctcattt tgcgcatggc ccacaagttc ataactggaa agctggtaga agatgaacgc   1020

agtgaccggg aagaaacaga gagctcagag ggggaggagg ctgcagctgg gggaggagca   1080

aagagccggc ccctagccaa tggccacccc atcctcaata acaaccatcg taagaatgac   1140

<210> 15

<211> 1755

<212> DNA

<213> Homo sapiens

<400> 15

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tgtgtgtctg	tggtggtcat	tgccgcaata	gtccttgcca	tcaccctgcg	gcggccaggc	120
tgtgagctgg	aggcctgcag	ccctgatgcc	gacatgctgg	actacctgct	gagcctgggc	180
cagatcagcc	ggcgagatgc	cttggaggtc	acctggtacc	acgcagccaa	cagcaagaaa	240
gccatgacag	ctgccctgaa	cagcaacatc	acagtcctgg	aggctgacgt	caatgtagaa	300
gggctcggca	cagccaatga	gacaggagtt	cccatcatgg	cacaccccccc	cactatctac	360
agtgacaaca	cactggagca	gtggctggac	gctgtgctgg	ctcttccca	aaagggcatc	420
aaactggact	tcaagaacat	caaggcagtg	ggcccctccc	tggacctcct	gcggcagctg	480
acagaggaag	gcaaagtccg	gcggcccata	tggatcaacg	ctgacatctt	aaagggcccc	540
aacatgctca	tctcaactga	ggtcaatgcc	acacagttcc	tggccctggt	ccaggagaag	600
tatcccaagg	ctaccctatc	tccaggctgg	accaccttct	acatgtccac	gtccccaaac	660
aggacgtaca	cccaagccat	ggtggagaag	atgacgagc	tggtgggagg	agtgccccag	720
agggtcacct	tccctgtacg	gtcttccatg	gtgcgggctg	cctggcccca	cttcagctgg	780
ctgctgagcc	aatctgagag	gtacagcctg	acgctgtggc	aggctgcctc	ggaccccatg	840
tcggtggaag	atctgctcta	cgtccgggat	aacactgctg	tccaccaagt	ctactatgac ·	900
atctttgagc	ctctcctgtc	acagttcaag	cagctggcct	tgaatgccac	acggaaacca	960
atgtactaca	caggaggcag	cctgatccct	cttctccagc	tgcctgggga	tgacggtctg	1020
aatgtggagt	ggctggttcc	tgacgtccag	ggcagcggta	aaacagcaac	aatgaccctc	1080
ccagacacag	aaggcatgat	cctgctgaac	actggcctcg	agggaactgt	ggctgaaaac	1140
cccgtgccca	ttgttcatac	tccaagtggc	aacatcctga	cgctggagtc	ctgcctgcag	1200
cagctggcca	cacatcccgg	acactggggc	atccatttgc	aaatagcgga	gcccgcagcc	1260
ctccggccat	ccctggcctt	gctggcacgc	ctctccagcc	ttggcctctt	gcattggcct	1320
gtgtgggttg	gggccaaaat	ctcccacggg	agtttttcgg	tccccggcca	tgtggctggc	1380
agagagctgc	ttacagctgt	ggctgaggtc	ttccccccacg	tgactgtggc	accaggctgg	1440

```
cctgaggagg  tgctgggcag  tggctacagg  gaacagctgc  tcacagatat  gctagagttg   1500

tgccaggggc  tctggcaacc  tgtgtccttc  cagatgcagg  ccatgctgct  gggccacagc   1560

acagctggag  ccataggcag  gctgctggca  tcctcccccc  gggccaccgt  cacagtggag   1620

cacaacccag  ctgggggcga  ctatgcctct  gtgaggacag  cattgctggc  agctagggct   1680

gtggacagga  cccgagtcta  ctacaggcta  ccccagggct  accacaagga  cttgctggct   1740

catgttggta  gaaac                                                       1755
```


<210> 16

<211> 993

<212> DNA

<213> Homo sapiens

<400> 16

```
atgtggctgt  gggaggacca  gggcggcctc  ctgggccctt  tctccttcct  gctgctagtg    60

ctgctgctgg  tgacgcggag  cccggtcaat  gcctgcctcc  tcaccggcag  cctcttcgtt   120

ctactgcgcg  tcttcagctt  tgagccggtg  ccctcttgca  gggccctgca  ggtgctcaag   180

ccccgggacc  gcatttctgc  catcgcccac  cgtggcggca  gccacgacgc  gcccgagaac   240

acgctggcgg  ccattcggca  ggcagctaag  aatggagcaa  caggcgtgga  gttggacatt   300

gagtttactt  ctgacgggat  tcctgtctta  atgcacgata  acacagtaga  taggacgact   360

gatgggactg  ggcgattgtg  tgatttgaca  tttgaacaaa  ttaggaagct  gaatcctgca   420

gcaaaccaca  gactcaggaa  tgatttccct  gatgaaaaga  tccctaccct  aagggaagct   480

gttgcagagt  gcctaaacca  taacctcaca  atcttctttg  atgtcaaagg  ccatgcacac   540

aaggctactg  aggctctaaa  gaaaatgtat  atggaatttc  ctcaactgta  taataatagt   600

gtggtctgtt  ctttcttgcc  agaagttatc  tacaagatga  gacaaacaga  tcgggatgta   660

ataacagcat  taactcacag  accttggagc  ctaagccata  caggagatgg  gaaaccacgc   720

tatgatactt  tctggaaaca  ttttatattt  gttatgatgg  acattttgct  cgattggagc   780
```

```
atgcataata tcttgtggta cctgtgtgga atttcagctt tcctcatgca aaaggatttt    840

gtatccccgg cctacttgaa gaagtggtca gctaaaggaa tccaggttgt tggttggact    900

gttaatacct ttgatgaaaa gagttactac gaatcccatc ttggttccag ctatatcact    960

gacagcatgg tagaagactg cgaacctcac ttc                                993
```

<210> 17

<211> 1035

<212> DNA

<213> Homo sapiens

<400> 17

```
atgtcgcctg aagaatggac gtatctagtg gttcttctta tctccatccc catcggcttc    60

ctctttaaga aagccggtcc tgggctgaag agatggggag cagccgctgt gggcctgggg    120

ctcaccctgt tcacctgtgg cccccacact ttgcattctc tggtcaccat cctcgggacc    180

tgggccctca ttcaggccca gccctgctcc tgccacgccc tggctctggc ctggactttc    240

tcctatctcc tgttcttccg agccctcagc ctcctgggcc tgcccactcc cacgcccttc    300

accaatgccg tccagctgct gctgacgctg aagctggtga gcctggccag tgaagtccag    360

gacctgcatc tggcccagag gaaggaaatg gcctcaggct tcagcaaggg gcccaccctg    420

gggctgctgc ccgacgtgcc ctccctgatg gagacactca gctacagcta ctgctacgtg    480

ggaatcatga caggcccgtt cttccgctac cgcacctacc tggactggct ggagcagccc    540

ttccccgggg cagtgcccag cctgcggccc ctgctgcgcc gcgcctggcc ggccccgctc    600

ttcggcctgc tgttcctgct ctcctctcac ctcttcccgc tggaggccgt gcgcgaggac    660

gccttctacg cccgcccgct gcccgcccgc ctcttctaca tgatccccgt cttcttcgcc    720

ttccgcatgc gcttctacgt ggcctggatt gccgccgagt gcggctgcat tgccgccggc    780

tttggggcct accccgtggc cgccaaagcc cgggccggag gcggccccac cctccaatgc    840

ccaccccccca gcagtccgga gaaggcggct tccttggagt atgactatga gaccatccgc    900
```

```
aacatcgact gctacagcac agatttctgc gtgcgggtgc gcgatggcat gcggtactgg    960

aacatgacgg tgcagtggtg gctggcgcag tatatctaca agagcgcacc tgcccgttcc    1020

tatgtcctgc gcctt                                                     1035
```

<210> 18

<211> 267

<212> DNA

<213> Homo sapiens

<400> 18

```
atgtacatgc aagattattg gaggacctgg ctcaaggggc tgcgcggctt cttcttcgtg    60

ggcgtcctct tctcggccgt ctccatcgct gccttctgca ccttcctcgt gctggccatc    120

acccggcatc agagcctcac agaccccacc agctactacc tctccagcgt ctggagcttc    180

atttccttca gtgggccttt cctgctcagc ctctatgccc accgctaccg ggctgacttt    240

gctgacatca gcatcctcag cgatttc                                        267
```

<210> 19

<211> 1218

<212> DNA

<213> Homo sapiens

<400> 19

```
atgcgcggct ctgtggagtg cacctggggt tggggcact gtgcccccag ccccctgctc    60

ctttggactc tacttctgtt tgcagcccca tttggcctgc tggggagaa gacccgccag    120

gtgtctctgg aggtcatccc taactggctg gcccccctgc agaacctgct tcatatacgg    180

gcagtgggca ccaattccac actgcactat gtgtggagca gcctggggcc tctggcagtg    240

gtaatggtgg ccaccaacac cccccacagc accctgagcg tcaactggag cctcctgcta    300
```

```
tcccctgagc ccgatggggg cctgatggtg ctccctaagg acagcattca gttttcttct   360

gcccttgttt ttaccaggct gcttgagttt gacagcacca acgtgtccga tacggcagca   420

aagcctttgg gaagaccata tcctccatac tccttggccg atttctcttg gaacaacatc   480

actgattcat tggatcctgc caccctgagt gccacatttc aaggccaccc catgaacgac   540

cctaccagga cttttgccaa tggcagcctg gccttcaggg tccaggcctt ttccaggtcc   600

agccgaccag cccaaccccc tcgcctcctg cacacagcag acacctgtca gctagaggtg   660

gccctgattg gagcctctcc ccggggaaac cgttccctgt ttgggctgga ggtagccaca   720

ttgggccagg gccctgactg cccctcaatg caggagcagc actccatcga cgatgaatat   780

gcaccggccg tcttccagtt ggaccagcta ctgtggggct ccctcccatc aggctttgca   840

cagtggcgac cagtggctta ctcccagaag ccggggggcc gagaatcagc cctgccctgc   900

caagcttccc ctcttcatcc tgccttagca tactctcttc cccagtcacc cattgtccga   960

gccttctttg ggtcccagaa taacttctgt gccttcaatc tgacgttcgg ggcttccaca  1020

ggccctggct attgggacca acactacctc agctggtcga tgctcctggg tgtgggcttc  1080

cctccagtgg acggcttgtc cccactagtc ctgggcatca tggcagtggc cctgggtgcc  1140

ccagggctca tgctgctagg gggcggcttg gttctgctgc tgcaccacaa gaagtactca  1200

gagtaccagt ccataaat                                                 1218
```

```
<210> 20

<211> 576

<212> DNA

<213> Homo sapiens

<400> 20

atgactgccg tcggcgtgca ggcccagagg cctttgggcc aaaggcagcc ccgccggtcc    60

ttctttgaat ccttcatccg gaccctcatc atcacgtgtg tggccctggc tgtggtcctg   120

tcctcggtct ccatttgtga tgggcactgg ctcctggctg aggaccgcct cttcgggctc   180
```

```
tggcacttct gcaccaccac caaccagagt gtgccgatct gcttcagaga cctgggccag      240

gcccatgtgc ccgggctggc cgtgggcatg ggcctggtac gcagcgtggg cgccttggcc      300

gtggtggccg ccattttttgg cctggagttc ctcatggtgt cccagttgtg cgaggacaaa     360

cactcacagt gcaagtgggt catgggttcc atcctcctcc tggtgtcttt cgtcctctcc      420

tccggcgggc tcctgggttt tgtgatcctc ctcaggaacc aagtcacact catcggcttc      480

accctaatgt tttggtgcga attcactgcc tccttcctcc tcttcctgaa cgccatcagc      540

ggccttcaca tcaacagcat cacccatccc tgggaa                                576
```

<210> 21

<211> 2042

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)... (894)

<400> 21

```
tccggtgcct gcagagctcg gagcggcgga ggcagagacc gaggctgcac cggcagaggc      60

tgcggggcgg acgcgcgggc cggcgcagcc atg gtg aag att agc ttc cag           111
                                    Met Val Lys Ile Ser Phe Gln
                                    1               5

ccc gcc gtg gct ggc atc aag ggc gac aag gct gac aag gcg tcg gcg        159
Pro Ala Val Ala Gly Ile Lys Gly Asp Lys Ala Asp Lys Ala Ser Ala
        10              15              20

tcg gcc cct gcg ccg gcc tcg gcc acc gag atc ctg ctg acg ccg gct        207
Ser Ala Pro Ala Pro Ala Ser Ala Thr Glu Ile Leu Leu Thr Pro Ala
```

```
                25                      30                      35
agg gag gag cag ccc cca caa cat cga tcc aag agg ggg agc tca gtg     255
Arg Glu Glu Gln Pro Pro Gln His Arg Ser Lys Arg Gly Ser Ser Val

        40                      45                      50          55
ggc ggc gtg tgc tac ctg tcg atg ggc atg gtc gtg ctg ctc atg ggc     303
Gly Gly Val Cys Tyr Leu Ser Met Gly Met Val Val Leu Leu Met Gly

                        60                      65              70
ctc gtg ttc gcc tct gtc tac atc tac aga tac ttc ttt ctt gca cag     351
Leu Val Phe Ala Ser Val Tyr Ile Tyr Arg Tyr Phe Phe Leu Ala Gln

                75                      80                      85
ctg gcc cga gat aac ttc ttc cgc tgt ggt gtg ctg tat gag gac tcc     399
Leu Ala Arg Asp Asn Phe Phe Arg Cys Gly Val Leu Tyr Glu Asp Ser

                        90                      95              100
ctg tcc tcc cag gtc cgg act cag atg gag ctg gaa gag gat gtg aaa     447
Leu Ser Ser Gln Val Arg Thr Gln Met Glu Leu Glu Glu Asp Val Lys

        105                     110                     115
atc tac ctc gac gag aac tac gag cgc atc aac gtg cct gtg ccc cag     495
Ile Tyr Leu Asp Glu Asn Tyr Glu Arg Ile Asn Val Pro Val Pro Gln
120                     125                     130             135
ttt ggc ggc ggt gac cct gca gac atc atc cat gac ttc cag cgg ggt     543
Phe Gly Gly Gly Asp Pro Ala Asp Ile Ile His Asp Phe Gln Arg Gly

                140                     145                     150
ctg act gcg tac cat gat atc tcc ctg gac aag tgc tat gtc atc gaa     591
Leu Thr Ala Tyr His Asp Ile Ser Leu Asp Lys Cys Tyr Val Ile Glu

                155                     160                     165
```

```
ctc aac acc acc att gtg ctg ccc cct cgc aac ttc tgg gag ctc ctc     639
Leu Asn Thr Thr Ile Val Leu Pro Pro Arg Asn Phe Trp Glu Leu Leu
        170                 175                 180

atg aac gtg aag agg ggg acc tac ctg ccg cag acg tac atc atc cag     687
Met Asn Val Lys Arg Gly Thr Tyr Leu Pro Gln Thr Tyr Ile Ile Gln
        185                 190                 195

gag gag atg gtg gtc acg gag cat gtc agt gac aag gag gcc ctg ggg     735
Glu Glu Met Val Val Thr Glu His Val Ser Asp Lys Glu Ala Leu Gly
200                 205                 210                 215

tcc ttc atc tac cac ctg tgc aac ggg aaa gac acc tac cgg ctc cgg     783
Ser Phe Ile Tyr His Leu Cys Asn Gly Lys Asp Thr Tyr Arg Leu Arg
                    220                 225                 230

cgc cgg gca acg cgg agg cgg atc aac aag cgt ggg gcc aag aac tgc     831
Arg Arg Ala Thr Arg Arg Arg Ile Asn Lys Arg Gly Ala Lys Asn Cys
                235                 240                 245

aat gcc atc cgc cac ttc gag aac acc ttc gtg gtg gag acg ctc atc     879
Asn Ala Ile Arg His Phe Glu Asn Thr Phe Val Val Glu Thr Leu Ile
        250                 255                 260

tgc ggg gtg gtg tgaggccctc ctcccccaga accccctgcc gtgttcctc         930
Cys Gly Val Val
        265

ttttcttctt tccggctgct ctctggccct cctccttccc cctgcttagc ttgtactttg  990

gacgcgtttc tatagaggtg acatgtctct ccattcctct ccaaccctgc ccacctccct  1050

gtaccagagc tgtgatctct cggtgggggg cccatctctg ctgacctggg tgtggcggag  1110

ggagaggcga tgctgcaaag tgttttctgt gtcccactgt cttgaagctg ggcctgccaa  1170
```

```
agcctgggcc  cacagctgca  ccggcagccc  aaggggaagg  accggttggg  ggagccgggc   1230

atgtgaggcc  ctgggcaagg  ggatgggggct  gtggggggcgg  ggcggcatgg  gcttcagaag   1290

tatctgcaca  attagaaaag  tcctcagaag  cttttttcttg  gagggtacac  tttcttcact   1350

gtccctattc  ctagacctgg  ggcttgagct  gaggatggga  cgatgtgccc  agggagggac   1410

ccaccagagc  acaagagaag  gtggctacct  gggggtgtcc  cagggactct  gtcagtgcct   1470

tcagcccacc  agcaggagct  tggagtttgg  ggagtggggga  tgagtccgtc  aagcacaact   1530

gttctctgag  tggaaccaaa  gaagcaagga  gctaggaccc  ccagtcctgc  cccccaggag   1590

cacaagcagg  gtcccctcag  tcaaggcagt  gggatgggcg  gctgaggaac  ggggcaggca   1650

aggtcactgc  tcagtcacgt  ccacggggga  cgagccgtgg  gttctgctga  gtaggtggag   1710

ctcattgctt  tctccaagct  tggaactgtt  ttgaaagata  acacagaggg  aaagggagag   1770

ccacctggta  cttgtccacc  ctgcctcctc  tgttctgaaa  ttccatcccc  ctcagcttag   1830

gggaatgcac  cttttttccct  ttccttctca  cttttgcatg  tttttactga  tcattcgata   1890

tgctaaccgt  tctcagccct  gagccttgga  gaggagggct  gtaacgcctt  cagtcagtct   1950

ctggggatga  aactcttaaa  tgctttgtat  attttctcaa  ttagatctct  tttcagaagt   2010

gtctatagaa  caataaaaat  cttttacttc  tg                                   2042
```

<210> 22

<211> 1433

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (5)... (1264)

<400> 22

```
gacg atg agc tgc gcg ggg cgg gcg ggc cct gcc cgg ctc gcc gcg              46
     Met Ser Cys Ala Gly Arg Ala Gly Pro Ala Arg Leu Ala Ala
```

```
        1              5                 10

ctc gcc ctg ctg acc tgc agc ctg tgg ccg gca cgg gca gac aac gcg        94
Leu Ala Leu Leu Thr Cys Ser Leu Trp Pro Ala Arg Ala Asp Asn Ala
      15             20                25                30

agc cag gag tac tac acg gcg ctc atc aac gtg acg gtg cag gag ccc       142
Ser Gln Glu Tyr Tyr Thr Ala Leu Ile Asn Val Thr Val Gln Glu Pro
                  35                40                45

ggc cgc ggc gcc ccg ctc acg ttt cgc atc gac cgc ggg cgc tac ggg       190
Gly Arg Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg Gly Arg Tyr Gly
            50                55                60

ctt gac tcc ccc aag gcc gag gtc cgc ggc cag gtg ctg gcg ccg ctg       238
Leu Asp Ser Pro Lys Ala Glu Val Arg Gly Gln Val Leu Ala Pro Leu
            65                70                75

ccc ctc cac gga gtt gct gat cat ctg ggc tgt gat cca caa acc cgg       286
Pro Leu His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg
            80                85                90

ttc ttt gtc cct cct aat atc aaa cag tgg att gcc ttg ctg cag agg       334
Phe Phe Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg
95                100                105                110

gga aac tgc acg ttt aaa gag aaa ata tca cgg gcc gct ttc cac aat       382
Gly Asn Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn
                  115                120                125

gca gtt gct gta gtc atc tac aat aat aaa tcc aaa gag gag cca gtt       430
Ala Val Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val
            130                135                140
```

acc atg act cat cca ggc act gga gat att att gct gtc atg ata aca   478
Thr Met Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr
        145   150   155

gaa ttg agg ggt aag gat att ttg agt tat ctg gag aaa aac atc tct   526
Glu Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser
        160   165   170

gta caa atg aca ata gct gtt gga act cga atg cca ccg aag aac ttc   574
Val Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe
175   180   185   190

agc cgt ggc tct cta gtc ttc gtg tca ata tcc ttt att gtt ttg atg   622
Ser Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met
        195   200   205

att att tct tca gca tgg ctc ata ttc tac ttc att cag aag atc agg   670
Ile Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg
        210   215   220

tac aca aat gca cgc gac agg aac cag cgt cgt ctc gga gat gca gcc   718
Tyr Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala
        225   230   235

aag aaa gcc atc agt aaa ttg aca acc agg aca gta aag aag ggt gac   766
Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp
        240   245   250

aag gaa act gac cca gac ttt gat cat tgt gca gtc tgc ata gag agc   814
Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser
255   260   265   270

tat aag cag aat gat gtc gtc cga att ctc ccc tgc aag cat gtt ttc   862

Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe
            275   280   285

cac aaa tcc tgc gtg gat ccc tgg ctt agt gaa cat tgt acc tgt cct   910
His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro
            290   295   300

atg tgc aaa ctt aat ata ttg aag gcc ctg gga att gtg ccg aat ttg   958
Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu
            305   310   315

cca tgt act gat aac gta gca ttc gat atg gaa agg ctc acc aga acc   1006
Pro Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr
            320   325   330

caa gct gtt aac cga aga tca gcc ctc ggc gac ctc gcc ggc gac aac   1054
Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn
335   340   345   350

tcc ctt ggc ctt gag cca ctt cga act tcg ggg atc tca cct ctt cct   1102
Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro
            355   360   365

cag gat ggg gag ctc act ccg aga aca gga gaa atc aac att gca gta   1150
Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val
            370   375   380

aca aaa gaa tgg ttt att att gcc agt ttt ggc ctc ctc agt gcc ctc   1198
Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu
            385   390   395

aca ctc tgc tac atg atc atc aga gcc aca gct agc ttg aat gct aat   1246
Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn

400   405   410

gag gta gaa tgg ttt tgaagaagaa aaaacctgct ttctgactga ttttgcctt   1300

Glu Val Glu Trp Phe

415

gaaggaaaaa agaacctatt tttgtgcatc atttaccaat catgccacac aagcatttat   1360

ttttagtaca ttttattttt tcataaaatt gctaatgcca aagctttgta ttaaaagaaa   1420

taaataataa aat   1433

<210> 23

<211> 1917

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210)... (1457)

<400> 23

gtatcccccg gctacctggg ccgccccgcg gcggtgcgcg cgtgagaggg agcgcgcggg   60

cagccgagcg ccggtgtgag ccagcgctgc tgccagtgtg agccagcgct gctgccagtg   120

tgagcggcgg tgtgagcgcg gtgggtgcgg aggggcgtgt gtgccggcgc gcgcgccgtg   180

gggtgcaaac cccgagcgtc tacgctgcc atg agg ggc gcg aac gcc tgg gcg   233

                                  Met Arg Gly Ala Asn Ala Trp Ala

                                   1   5

cca ctc tgc ctg ctg ctg gct gcc gcc acc cag ctc tcg cgg cag cag   281

Pro Leu Cys Leu Leu Leu Ala Ala Ala Thr Gln Leu Ser Arg Gln Gln

    10   15   20

tcc cca gag aga cct gtt ttc aca tgt ggt ggc att ctt act gga gag   329

Ser Pro Glu Arg Pro Val Phe Thr Cys Gly Gly Ile Leu Thr Gly Glu

25   30   35   40

tct gga ttt att ggc agt gaa ggt ttt cct gga gtg tac cct cca aat   377

Ser Gly Phe Ile Gly Ser Glu Gly Phe Pro Gly Val Tyr Pro Pro Asn

45   50   55

agc aaa tgt act tgg aaa atc aca gtt ccc gaa gga aaa gta gtc gtt   425

Ser Lys Cys Thr Trp Lys Ile Thr Val Pro Glu Gly Lys Val Val Val

60   65   70

ctc aat ttc cga ttc ata gac ctc gag agt gac aac ctg tgc cgc tat   473

Leu Asn Phe Arg Phe Ile Asp Leu Glu Ser Asp Asn Leu Cys Arg Tyr

75   80   85

gac ttt gtg gat gtg tac aat ggc cat gcc aat ggc cag cgc att ggc   521

Asp Phe Val Asp Val Tyr Asn Gly His Ala Asn Gly Gln Arg Ile Gly

90   95   100

cgc ttc tgt ggc act ttc cgg cct gga gcc ctt gtg tcc agt ggc aac   569

Arg Phe Cys Gly Thr Phe Arg Pro Gly Ala Leu Val Ser Ser Gly Asn

105   110   115   120

aag atg atg gtg cag atg att tct gat gcc aac aca gct ggc aat ggc   617

Lys Met Met Val Gln Met Ile Ser Asp Ala Asn Thr Ala Gly Asn Gly

125   130   135

ttc atg gcc atg ttc tcc gct gct gaa cca aac gaa aga ggg gat cag   665

Phe Met Ala Met Phe Ser Ala Ala Glu Pro Asn Glu Arg Gly Asp Gln

140   145   150

tat tgt gga gga ctc ctt gac aga cct tcc ggc tct ttt aaa acc ccc   713

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                Tyr Cys Gly Gly Leu Leu Asp Arg Pro Ser Gly Ser Phe Lys Thr Pro
                        155             160             165

aac tgg cca gac cgg gat tac cct gca gga gtc act tgt gtg tgg cac        761
Asn Trp Pro Asp Arg Asp Tyr Pro Ala Gly Val Thr Cys Val Trp His
        170             175             180

att gta gcc cca aag aat cag ctt ata gaa tta aag ttt gag aag ttt       809
Ile Val Ala Pro Lys Asn Gln Leu Ile Glu Leu Lys Phe Glu Lys Phe
185             190             195             200

gat gtg gag cga gat aac tac tgc cga tat gat tat gtg gct gtg ttt       857
Asp Val Glu Arg Asp Asn Tyr Cys Arg Tyr Asp Tyr Val Ala Val Phe
                205             210             215

aat ggc ggg gaa gtc aac gat gct aga aga att gga aag tat tgt ggt       905
Asn Gly Gly Glu Val Asn Asp Ala Arg Arg Ile Gly Lys Tyr Cys Gly
                220             225             230

gat agt cca cct gcg cca att gtg tct gag aga aat gaa ctt ctt att       953
Asp Ser Pro Pro Ala Pro Ile Val Ser Glu Arg Asn Glu Leu Leu Ile
                235             240             245

cag ttt tta tca gac tta agt tta act gca gat ggg ttt att ggt cac      1001
Gln Phe Leu Ser Asp Leu Ser Leu Thr Ala Asp Gly Phe Ile Gly His
        250             255             260

tac ata ttc agg cca aaa aaa ctg cct aca act aca gaa cag cct gtc      1049
Tyr Ile Phe Arg Pro Lys Lys Leu Pro Thr Thr Thr Glu Gln Pro Val
265             270             275             280

acc acc aca ttc cct gta acc acg ggt tta aaa acc acc gtg gcc ttg      1097
Thr Thr Thr Phe Pro Val Thr Thr Gly Leu Lys Thr Thr Val Ala Leu
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                    285                  290                  295
tgt caa caa aag tgt aga cgg acg ggg act ctg gag ggc aat tat tgt      1145
Cys Gln Gln Lys Cys Arg Arg Thr Gly Thr Leu Glu Gly Asn Tyr Cys

                300                  305                  310
tca agt gac ttt gta tta gcc ggc act gtt atc aca acc atc act cgc      1193
Ser Ser Asp Phe Val Leu Ala Gly Thr Val Ile Thr Thr Ile Thr Arg

            315                  320                  325
gat ggg agt ttg cac gcc aca gtc tcg atc atc aac atc tac aaa gag      1241
Asp Gly Ser Leu His Ala Thr Val Ser Ile Ile Asn Ile Tyr Lys Glu

        330                  335                  340
gga aat ttg gcg att cag cag gcg ggc aag aac atg agt gcc agg ctg      1289
Gly Asn Leu Ala Ile Gln Gln Ala Gly Lys Asn Met Ser Ala Arg Leu

345                  350                  355                  360
act gtc gtc tgc aag cag tgc cct ctc ctc aga aga ggt cta aat tac      1337
Thr Val Val Cys Lys Gln Cys Pro Leu Leu Arg Arg Gly Leu Asn Tyr

                365                  370                  375
att att atg ggc caa gta ggt gaa gat ggg cga ggc aaa atc atg cca      1385
Ile Ile Met Gly Gln Val Gly Glu Asp Gly Arg Gly Lys Ile Met Pro

            380                  385                  390
aac agc ttt atc atg atg ttc aag acc aag aat cag aag ctc ctg gat      1433
Asn Ser Phe Ile Met Met Phe Lys Thr Lys Asn Gln Lys Leu Leu Asp

        395                  400                  405
gcc tta aaa aat aag caa tgt taacagtgaa ctgtgtccat ttaagc            1480
Ala Leu Lys Asn Lys Gln Cys

    410                  415
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tgtattctgc cattgccttt gaaagatcta tgttctctca gtagaaaaaa aaatacttat    1540

aaaattacat attctgaaag aggattccga aagatgggac tggttgactc ttcacatgat    1600

ggaggtatga ggcctccgag atagctgagg gaagttcttt gcctgctgtc agaggagcag    1660

ctatctgatt ggaaacctgc cgacttagtg cggtgatagg aagctaaaag tgtcaagcgt    1720

tgacagcttg gaagcgttta tttatacatc tctgtaaaag gatattttag aattgagttg    1780

tgtgaagatg tcaaaaaaag attttagaag tgcaatattt atagtgttat ttgtttcacc    1840

ttcaagcctt tgccctgagg tgttacaatc ttgtcttgcg ttttctaaat caatgcttaa    1900

taaaatattt ttaaagg    1917
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ccgcggctgg cggaggaggg agggcgaggg cgggcgcggg ccggcgggcg ggcggaagag    120

ggaggagagg cgcggggagc caggcctcgg ggcctcggag caaccacccg agcagacgga    180

gtacacggag cagcggcccc ggccccgcca acgctgccgc cggg atg ctc cag    233
                                                  Met Leu Gln
                                                   1

acc ttg tat gat tac ttc tgg tgg gaa cgt ctg tgg ctg cct gtg aac    281
Thr Leu Tyr Asp Tyr Phe Trp Trp Glu Arg Leu Trp Leu Pro Val Asn
```

	5				10				15						

```
     5                    10                   15
ttg acc tgg gcc gat cta gaa gac cga gat gga cgt gtc tac gcc aaa      329
Leu Thr Trp Ala Asp Leu Glu Asp Arg Asp Gly Arg Val Tyr Ala Lys
     20                   25                   30                   35
gcc tca gat ctc tat atc acg ctg ccc ctg gcc ttg ctc ttc ctc atc      377
Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Leu Phe Leu Ile
                    40                   45                   50
gtt cga tac ttc ttt gag ctg tac gtg gct aca cca ctg gct gcc ctc      425
Val Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu Ala Ala Leu
                    55                   60                   65
ttg aac ata aag gag aaa act cgg ctg cgg gca cct ccc aac gcc acc      473
Leu Asn Ile Lys Glu Lys Thr Arg Leu Arg Ala Pro Pro Asn Ala Thr
                    70                   75                   80
ttg gaa cat ttc tac ctg acc agt ggc aag cag ccc aag cag gtg gaa      521
Leu Glu His Phe Tyr Leu Thr Ser Gly Lys Gln Pro Lys Gln Val Glu
               85                   90                   95
gta gag ctt ttg tcc cgg cag agc ggg ctc tct ggc cgc cag gta gag      569
Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg Gln Val Glu
100                  105                  110                  115
cgt tgg ttc cgt cgc cgc cgc aac cag gac cgg ccc agt ctc ctc aag      617
Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser Leu Leu Lys
                    120                  125                  130
aag ttc cga gaa gcc agc tgg aga ttc aca ttt tac ctg att gcc ttc      665
Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu Ile Ala Phe
                    135                  140                  145
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att gcc ggc atg gcc gtc att gtg gat aaa ccc tgg ttc tat gac atg   713
Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr Asp Met
            150   155   160

aag aaa gtt tgg gag gga tat ccc ata cag agc act atc cct tcc cag   761
Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro Ser Gln
        165   170   175

tat tgg tac tac atg att gaa ctt tcc ttc tac tgg tcc ctg ctc ttc   809
Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu Leu Phe
180   185   190   195

agc att gcc tct gat gtc aag cga aag gat ttc aag gaa cag atc atc   857
Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln Ile Ile
            200   205   210

cac cat gtg gcc acc atc att ctc atc agc ttt tcc tgg ttt gcc aat   905
His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe Ala Asn
            215   220   225

tac atc cga gct ggg act cta atc atg gct ctg cat gac tct tcc gat   953
Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser Ser Asp
            230   235   240

tac ctg ctg gag tca gcc aag atg ttt aac tac gcg gga tgg aag aac   1001
Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp Lys Asn
        245   250   255

acc tgc aac aac atc ttc atc gtc ttc gcc att gtt ttt atc atc acc   1049
Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe Ile Ile Thr
260   265   270   275

cga ctg gtc atc ctg ccc ttc tgg atc ctg cat tgc acc ctg gtg tac   1097

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Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr Leu Val Tyr
                280                 285                 290

cca ctg gag ctc tat cct gcc ttc ttt ggc tat tac ttc ttc aat tcc     1145
Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe Phe Asn Ser
                295                 300                 305

atg atg gga gtt cta cag ctg ctg cat atc ttc tgg gcc tac ctc att     1193
Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala Tyr Leu Ile
                310                 315                 320

ttg cgc atg gcc cac aag ttc ata act gga aag ctg gta gaa gat gaa     1241
Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val Glu Asp Glu
            325                 330                 335

cgc agt gac cgg gaa gaa aca gag agc tca gag ggg gag gag gct gca     1289
Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu Glu Ala Ala
340                 345                 350                 355

gct ggg gga gga gca aag agc cgg ccc cta gcc aat ggc cac ccc atc     1337
Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly His Pro Ile
                360                 365                 370

ctc aat aac aac cat cgt aag aat gac tgaaccatta ttccagctgc ctccca    1390
Leu Asn Asn Asn His Arg Lys Asn Asp
                375                 380

gattaatgca taaagccaag gaactaccct gctccctgcg ctatagggtc actttaagct   1450

ctggggaaaa aggagaaagt gagaggagag ttctctgcat cctccctcct tgcttgtcac   1510

ccagttgcct ttaaaccaaa ttctaaccag cctatcccca ggtaggggga cgttggttat   1570

attctgttag agggggacgg tcgtattttc ctccgtaccc gccaagtcat cctttctact   1630

gcttttgagg ccctccctca gctctctgtg ggtaggggtt acaattcaca ttccttattc   1690
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tgagaatttg gccccagctg tttgcctttg actccctgac ctccagagcc agggttgtgc   1750

cttattgtcc catctgtggg cctcattctg ccaaagctgg accaaggcta acctttctaa   1810

gctccctaac ttgggccaga aaccaaagct gagcttttaa ctttctccct ctatgacaca   1870

aatgaattga gggtaggagg agggtgcaca taacccttac cctacctctg ccaaaaagtg   1930

ggggctgtac tggggactgc tcggatgatc tttcttagtg ctacttcttt cagctgtccc   1990

tgtagcgaca ggtctaagat ctgactgcct cctttctctg gcctcttccc ccttccctct   2050

tctcttcagc taggctagct ggtttggagt agaatggcaa ctaattctaa tttttatatta   2110

ttaaatattt ggggttttgg ttttaaagcc agaattacgg ctagcaccta gcatttcagc   2170

agagggacca ttttagacca aaatgtactg ttaatgggtt ttttttttaaa attaaaagat   2230

taaataaaaa atattaaata aaacatgg   2258

<210> 25

<211> 1973

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (130)...(1887)

<400> 25

gagcagacca ggcccggtgg agaattaggt gctgctggga gctcctgcct cccacaggat   60

tccagctgca gggagcctca gggactctgg ccgcacgga gttgggggca ttccccagag   120

agcgtcgcc atg gtc tgc agg gag cag tta tca aag aat cag gtc aag   168

        Met Val Cys Arg Glu Gln Leu Ser Lys Asn Gln Val Lys
        1   5   10

tgg gtg ttt gcc ggc att acc tgt gtg tct gtg gtg gtc att gcc gca   216

Trp Val Phe Ala Gly Ile Thr Cys Val Ser Val Val Val Ile Ala Ala

15   20   25

ata gtc ctt gcc atc acc ctg cgg cgg cca ggc tgt gag ctg gag gcc   264

Ile Val Leu Ala Ile Thr Leu Arg Arg Pro Gly Cys Glu Leu Glu Ala

30   35   40   45

tgc agc cct gat gcc gac atg ctg gac tac ctg ctg agc ctg ggc cag   312

Cys Ser Pro Asp Ala Asp Met Leu Asp Tyr Leu Leu Ser Leu Gly Gln

50   55   60

atc agc cgg cga gat gcc ttg gag gtc acc tgg tac cac gca gcc aac   360

Ile Ser Arg Arg Asp Ala Leu Glu Val Thr Trp Tyr His Ala Ala Asn

65   70   75

agc aag aaa gcc atg aca gct gcc ctg aac agc aac atc aca gtc ctg   408

Ser Lys Lys Ala Met Thr Ala Ala Leu Asn Ser Asn Ile Thr Val Leu

80   85   90

gag gct gac gtc aat gta gaa ggg ctc ggc aca gcc aat gag aca gga   456

Glu Ala Asp Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr Gly

95   100   105

gtt ccc atc atg gca cac ccc ccc act atc tac agt gac aac aca ctg   504

Val Pro Ile Met Ala His Pro Pro Thr Ile Tyr Ser Asp Asn Thr Leu

110   115   120   125

gag cag tgg ctg gac gct gtg ctg ggc tct tcc caa aag ggc atc aaa   552

Glu Gln Trp Leu Asp Ala Val Leu Gly Ser Ser Gln Lys Gly Ile Lys

130   135   140

ctg gac ttc aag aac atc aag gca gtg ggc ccc tcc ctg gac ctc ctg   600

Leu Asp Phe Lys Asn Ile Lys Ala Val Gly Pro Ser Leu Asp Leu Leu

48 /307

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            145                 150                 155
cgg cag ctg aca gag gaa ggc aaa gtc cgg cgg ccc ata tgg atc aac     648
Arg Gln Leu Thr Glu Glu Gly Lys Val Arg Arg Pro Ile Trp Ile Asn
            160                 165                 170
gct gac atc tta aag ggc ccc aac atg ctc atc tca act gag gtc aat     696
Ala Asp Ile Leu Lys Gly Pro Asn Met Leu Ile Ser Thr Glu Val Asn
        175                 180                 185
gcc aca cag ttc ctg gcc ctg gtc cag gag aag tat ccc aag gct acc     744
Ala Thr Gln Phe Leu Ala Leu Val Gln Glu Lys Tyr Pro Lys Ala Thr
190                 195                 200                 205
cta tct cca ggc tgg acc acc ttc tac atg tcc acg tcc cca aac agg     792
Leu Ser Pro Gly Trp Thr Thr Phe Tyr Met Ser Thr Ser Pro Asn Arg
                210                 215                 220
acg tac acc caa gcc atg gtg gag aag atg cac gag ctg gtg gga gga     840
Thr Tyr Thr Gln Ala Met Val Glu Lys Met His Glu Leu Val Gly Gly
                225                 230                 235
gtg ccc cag agg gtc acc ttc cct gta cgg tct tcc atg gtg cgg gct     888
Val Pro Gln Arg Val Thr Phe Pro Val Arg Ser Ser Met Val Arg Ala
            240                 245                 250
gcc tgg ccc cac ttc agc tgg ctg ctg agc caa tct gag agg tac agc     936
Ala Trp Pro His Phe Ser Trp Leu Leu Ser Gln Ser Glu Arg Tyr Ser
        255                 260                 265
ctg acg ctg tgg cag gct gcc tcg gac ccc atg tcg gtg gaa gat ctg     984
Leu Thr Leu Trp Gln Ala Ala Ser Asp Pro Met Ser Val Glu Asp Leu
270                 275                 280                 285
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ctc tac gtc cgg gat aac act gct gtc cac caa gtc tac tat gac atc   1032
Leu Tyr Val Arg Asp Asn Thr Ala Val His Gln Val Tyr Tyr Asp Ile
             290   295   300

ttt gag cct ctc ctg tca cag ttc aag cag ctg gcc ttg aat gcc aca   1080
Phe Glu Pro Leu Leu Ser Gln Phe Lys Gln Leu Ala Leu Asn Ala Thr
             305   310   315

cgg aaa cca atg tac tac aca gga ggc agc ctg atc cct ctt ctc cag   1128
Arg Lys Pro Met Tyr Tyr Thr Gly Gly Ser Leu Ile Pro Leu Leu Gln
             320   325   330

ctg cct ggg gat gac ggt ctg aat gtg gag tgg ctg gtt cct gac gtc   1176
Leu Pro Gly Asp Asp Gly Leu Asn Val Glu Trp Leu Val Pro Asp Val
             335   340   345

cag ggc agc ggt aaa aca gca aca atg acc ctc cca gac aca gaa ggc   1224
Gln Gly Ser Gly Lys Thr Ala Thr Met Thr Leu Pro Asp Thr Glu Gly
350   355   360   365

atg atc ctg ctg aac act ggc ctc gag gga act gtg gct gaa aac ccc   1272
Met Ile Leu Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro
             370   375   380

gtg ccc att gtt cat act cca agt ggc aac atc ctg acg ctg gag tcc   1320
Val Pro Ile Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser
             385   390   395

tgc ctg cag cag ctg gcc aca cat ccc gga cac tgg ggc atc cat ttg   1368
Cys Leu Gln Gln Leu Ala Thr His Pro Gly His Trp Gly Ile His Leu
             400   405   410

caa ata gcg gag ccc gca gcc ctc cgg cca tcc ctg gcc ttg ctg gca   1416

Gln Ile Ala Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala

415   420   425

cgc ctc tcc agc ctt ggc ctc ttg cat tgg cct gtg tgg gtt ggg gcc   1464

Arg Leu Ser Ser Leu Gly Leu Leu His Trp Pro Val Trp Val Gly Ala

430   435   440   445

aaa atc tcc cac ggg agt ttt tcg gtc ccc ggc cat gtg gct ggc aga   1512

Lys Ile Ser His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg

                    450   455   460

gag ctg ctt aca gct gtg gct gag gtc ttc ccc cac gtg act gtg gca   1560

Glu Leu Leu Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala

                    465   470   475

cca ggc tgg cct gag gag gtg ctg ggc agt ggc tac agg gaa cag ctg   1608

Pro Gly Trp Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu

                    480   485   490

ctc aca gat atg cta gag ttg tgc cag ggg ctc tgg caa cct gtg tcc   1656

Leu Thr Asp Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser

                    495   500   505

ttc cag atg cag gcc atg ctg ctg ggc cac agc aca gct gga gcc ata   1704

Phe Gln Met Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile

510   515   520   525

ggc agg ctg ctg gca tcc tcc ccc cgg gcc acc gtc aca gtg gag cac   1752

Gly Arg Leu Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His

                    530   535   540

aac cca gct ggg ggc gac tat gcc tct gtg agg aca gca ttg ctg gca   1800

Asn Pro Ala Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala

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               545                550                555
gct agg gct gtg gac agg acc cga gtc tac tac agg cta ccc cag ggc      1848
Ala Arg Ala Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly
          560                565                570
tac cac aag gac ttg ctg gct cat gtt ggt aga aac tgagcaccca ggggtg    1900
Tyr His Lys Asp Leu Leu Ala His Val Gly Arg Asn
      575                580                585
gtgggccagc ggacctcagg gcggaggctt cccacgggga ggcaggaaga aataaaggtc    1960
tttggctttc tcc                                                       1973
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<211> 1606

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<213> Homo sapiens

<220>

<221> CDS

<222> (135)... (1130)

<400> 26

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cctcgcttct cgttctactg ccccaggagc ccggcgggtc cgggactccc gtccgtgccg    120
gtgcgggcgc cggc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc     170
                Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly
                1                5                  10
cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg     218
Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro
```

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                   15                    20                    25
gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc      266
Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val
       30                    35                    40
ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag      314
Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys
   45                    50                    55                    60
ccc cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac      362
Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp
                   65                    70                    75
gcg ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga      410
Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly
       80                    85                    90
gca aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct      458
Ala Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro
       95                    100                   105
gtc tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg      506
Val Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly
       110                   115                   120
cga ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca      554
Arg Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala
125                   130                   135                   140
gca aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc      602
Ala Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr
                   145                   150                   155
```

```
cta agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc        650
Leu Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe
            160                 165                 170

ttt gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa        698
Phe Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys
            175                 180                 185

atg tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct        746
Met Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser
        190                 195                 200

ttc ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta        794
Phe Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val
205                210                 215                 220

ata aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat        842
Ile Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp
                225                 230                 235

ggg aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg        890
Gly Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met
                240                 245                 250

atg gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg        938
Met Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu
            255                 260                 265

tgt gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc        986
Cys Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala
        270                 275                 280

tac ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act       1034
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Tyr Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr

285   290   295   300

gtt aat acc ttt gat gaa aag agt tac tac gaa tcc cat ctt ggt tcc   1082

Val Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser

                    305   310   315

agc tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc   1127

Ser Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe

            320   325   330

tag actttcacgg tgggacgaaa cgggttcaga aactgccagg ggcctcatac   1180

agggatatca aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca   1240

aatgcaatag ttggtcactg catttttacc tgaaccaaag ctaaacccgg tgttgccacc   1300

atgcaccatg gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa   1360

cgcacaagag cccctgccct gccctagctg aggcacacag ggagacccag tgaggataag   1420

cacagattga attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcatgataa   1480

ctcagagttg acattttaaa acttgccaca cttatttcaa atatttgtac tcagctatgt   1540

taacatgtac tgtagacatc aaacttgtgg ccatactaat aaaattatta aaaggagcac   1600

taaagg   1606

<210> 27

<211> 2380

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (247)... (1284)

<400> 27

agtgtggacc tggactcgaa tcccgttgcc gactcgcgct ctcggcttct gctccggggc   60

ttcttccctg cccgcccggg gccctgaccg tggcttcttc cccggcctga tctgcgcagc   120

ccggcgggcg cccagaagga gcaggcggcg cgggggcgcg ctgggcgggg gaggcgtggc   180

cggagctgcg gcggcaagcg ggctgggact gctcggccgc ctcctgcccg gcgagcagct   240

cagacc atg tcg cct gaa gaa tgg acg tat cta gtg gtt ctt ctt atc   288

       Met Ser Pro Glu Glu Trp Thr Tyr Leu Val Val Leu Leu Ile

        1   5   10

tcc atc ccc atc ggc ttc ctc ttt aag aaa gcc ggt cct ggg ctg aag   336

Ser Ile Pro Ile Gly Phe Leu Phe Lys Lys Ala Gly Pro Gly Leu Lys

 15   20   25   30

aga tgg gga gca gcc gct gtg ggc ctg ggg ctc acc ctg ttc acc tgt   384

Arg Trp Gly Ala Ala Ala Val Gly Leu Gly Leu Thr Leu Phe Thr Cys

              35   40   45

ggc ccc cac act ttg cat tct ctg gtc acc atc ctc ggg acc tgg gcc   432

Gly Pro His Thr Leu His Ser Leu Val Thr Ile Leu Gly Thr Trp Ala

              50   55   60

ctc att cag gcc cag ccc tgc tcc tgc cac gcc ctg gct ctg gcc tgg   480

Leu Ile Gln Ala Gln Pro Cys Ser Cys His Ala Leu Ala Leu Ala Trp

              65   70   75

act ttc tcc tat ctc ctg ttc ttc cga gcc ctc agc ctc ctg ggc ctg   528

Thr Phe Ser Tyr Leu Leu Phe Phe Arg Ala Leu Ser Leu Leu Gly Leu

              80   85   90

ccc act ccc acg ccc ttc acc aat gcc gtc cag ctg ctg ctg acg ctg   576

Pro Thr Pro Thr Pro Phe Thr Asn Ala Val Gln Leu Leu Leu Thr Leu

```
        95                   100                 105                 110
aag ctg gtg agc ctg gcc agt gaa gtc cag gac ctg cat ctg gcc cag          624
Lys Leu Val Ser Leu Ala Ser Glu Val Gln Asp Leu His Leu Ala Gln

                      115                 120                 125
agg aag gaa atg gcc tca ggc ttc agc aag ggg ccc acc ctg ggg ctg          672
Arg Lys Glu Met Ala Ser Gly Phe Ser Lys Gly Pro Thr Leu Gly Leu

                      130                 135                 140
ctg ccc gac gtg ccc tcc ctg atg gag aca ctc agc tac agc tac tgc          720
Leu Pro Asp Val Pro Ser Leu Met Glu Thr Leu Ser Tyr Ser Tyr Cys

                      145                 150                 155
tac gtg gga atc atg aca ggc ccg ttc ttc cgc tac cgc acc tac ctg          768
Tyr Val Gly Ile Met Thr Gly Pro Phe Phe Arg Tyr Arg Thr Tyr Leu

                      160                 165                 170
gac tgg ctg gag cag ccc ttc ccc ggg gca gtg ccc agc ctg cgg ccc          816
Asp Trp Leu Glu Gln Pro Phe Pro Gly Ala Val Pro Ser Leu Arg Pro

        175                 180                 185                 190
ctg ctg cgc cgc gcc tgg ccg gcc ccg ctc ttc ggc ctg ctg ttc ctg          864
Leu Leu Arg Arg Ala Trp Pro Ala Pro Leu Phe Gly Leu Leu Phe Leu

                      195                 200                 205
ctc tcc tct cac ctc ttc ccg ctg gag gcc gtg cgc gag gac gcc ttc          912
Leu Ser Ser His Leu Phe Pro Leu Glu Ala Val Arg Glu Asp Ala Phe

                      210                 215                 220
tac gcc cgc ccg ctg ccc gcc cgc ctc ttc tac atg atc ccc gtc ttc          960
Tyr Ala Arg Pro Leu Pro Ala Arg Leu Phe Tyr Met Ile Pro Val Phe

                      225                 230                 235
```

```
ttc gcc ttc cgc atg cgc ttc tac gtg gcc tgg att gcc gcc gag tgc     1008
Phe Ala Phe Arg Met Arg Phe Tyr Val Ala Trp Ile Ala Ala Glu Cys
     240               245              250

ggc tgc att gcc gcc ggc ttt ggg gcc tac ccc gtg gcc gcc aaa gcc     1056
Gly Cys Ile Ala Ala Gly Phe Gly Ala Tyr Pro Val Ala Ala Lys Ala
255               260              265              270

cgg gcc gga ggc ggc ccc acc ctc caa tgc cca ccc ccc agc agt ccg     1104
Arg Ala Gly Gly Gly Pro Thr Leu Gln Cys Pro Pro Pro Ser Ser Pro
               275              280              285

gag aag gcg gct tcc ttg gag tat gac tat gag acc atc cgc aac atc     1152
Glu Lys Ala Ala Ser Leu Glu Tyr Asp Tyr Glu Thr Ile Arg Asn Ile
          290              295              300

gac tgc tac agc aca gat ttc tgc gtg cgg gtg cgc gat ggc atg cgg     1200
Asp Cys Tyr Ser Thr Asp Phe Cys Val Arg Val Arg Asp Gly Met Arg
          305              310              315

tac tgg aac atg acg gtg cag tgg tgg ctg gcg cag tat atc tac aag     1248
Tyr Trp Asn Met Thr Val Gln Trp Trp Leu Ala Gln Tyr Ile Tyr Lys
     320              325              330

agc gca cct gcc cgt tcc tat gtc ctg cgc ctt tagaagcaga aactcagcc     1300
Ser Ala Pro Ala Arg Ser Tyr Val Leu Arg Leu
335               340              345

gggtgcggcg gctcacgcct ggaatcccag cactttggga ggcccaagca ggtggatcat     1360

gaggagcgcc tggaccatgc tgctgagcgc ctactggcac ggcctccacc cgggctacta     1420

cctgagcttc ctgaccatcc cgctgtgcct ggctgccgag ggccggctgg agtcagccct     1480

gcggggcggg ctgagcccag ggggccagaa ggcctgggac tgggtgcact ggttcctgaa     1540
```

```
gatgcgcgcc tatgactaca tgtgcatggg cttcgtgctg ctctccttgg ccgacaccct   1600

tcggtactgg gcctccatct acttctgtat ccacttcctg gccctggcag ccctggggct   1660

ggggctggct ttaggtgggg gcagccccag ccggcggaag gcagcatccc agcccaccag   1720

ccttgccccg gagaagctcc gggaggagta agctgtcacg acgctccctc tgccagctgg   1780

tcccgggaat tctgtgaacc aggctgctgt ctcctcccca gaaagagtcc ttaccttgga   1840

gagggtcctg gagagaattt cctcttcccc agctaaatac cctgcctgca actgaagcag   1900

acccgggggt gtcctccctg ccctctgccc agaggccacc tccactccta caaaatcaaa   1960

gtattgtcca dacaagagtc actggcccct gctccagctt ctgggtatcc agagagcact   2020

gcacttcccc aaaacggaag gggcccctgg gcagtgggtt ttgggcaaat tccctttctt   2080

tgcatccaca atgtggggtc ggagcttggg ggcaggtcct gggagtggga agcctcttcc   2140

ttgtgtcttt cgctccactt ttagctcatc gcaccaatat tgcagacttg gaaggaagca   2200

taagcttccc atttcacaaa ggggaaactg aggtgcgggt gcgcgggcct ggggacggcc   2260

gtcccatggc ttccatctga gccacctcgg daccccagca ctcctggcgc cctcttctca   2320

tcgcttggcc tatgacaggt caccgtgtgt aaatctttcc caataaagtg ttgcacaaag   2380
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<210> 28

<211> 2017

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (360)... (629)

<400> 28

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tccacacatt aagaaacgct ggtggagttt taaatgcctc tccggggaag gaggaaagcc      60

tgagaatgaa tctgacctca gacccaaatc cattcaacgg agttctggta atttggaaga     120
```

```
aggaagagca acctggaaac tgacaggaaa ggatgacaag ttgggagtca caggtatatg    180

atgggcctcc ccatgtggat ccttagtgct gtggcagagc ccttgttatt gtgctgggat    240

tttccctcca gctcccggcc ggaagctggg ctcacgtggg agctcagtgc cctcctgcta    300

cagatctgtc tcttccttac aatggggtgc tggcactgtg ggtcctggtg acgcacgtg    359
```

```
atg tac atg caa gat tat tgg agg acc tgg ctc aag ggg ctg cgc ggc    407
Met Tyr Met Gln Asp Tyr Trp Arg Thr Trp Leu Lys Gly Leu Arg Gly
 1           5                    10                   15

ttc ttc ttc gtg ggc gtc ctc ttc tcg gcc gtc tcc atc gct gcc ttc    455
Phe Phe Phe Val Gly Val Leu Phe Ser Ala Val Ser Ile Ala Ala Phe
             20                   25                   30

tgc acc ttc ctc gtg ctg gcc atc acc cgg cat cag agc ctc aca gac    503
Cys Thr Phe Leu Val Leu Ala Ile Thr Arg His Gln Ser Leu Thr Asp
         35                   40                   45

ccc acc agc tac tac ctc tcc agc gtc tgg agc ttc att tcc ttc aag    551
Pro Thr Ser Tyr Tyr Leu Ser Ser Val Trp Ser Phe Ile Ser Phe Lys
     50                   55                   60

tgg gcc ttc ctg ctc agc ctc tat gcc cac cgc tac cgg gct gac ttt    599
Trp Ala Phe Leu Leu Ser Leu Tyr Ala His Arg Tyr Arg Ala Asp Phe
 65              70                   75              80

gct gac atc agc atc ctc agc gat ttc tgacccaggg ggtg              640
Ala Asp Ile Ser Ile Leu Ser Asp Phe
             85
```

```
aggtctctgc accctggggg ggccttagga cctggactca gcctctgaga tgttgggaga    700

ggctactccc accccctggt gaccccagaa ctgtggcaga aaatacacag caggacgagt    760

gtggtctccc aggaagctgt cctgcccgtc ccctttcgag gaaacctgag tgtggtagag    820
```

```
aggggatcct gccatgttgt tcctcatcag cctggccaga gggcagcttt agaccttttc    880

aaatgaatct gttttctttt ctttcttttt tttttctttt tttttttttt ttgagatgga    940

gtcttactct gtcacccagg ctggagtgca gtagtgcgat ctcagctcac tgcaacctcc   1000

gcctcccagg ttcaagcaat tctcctgcct tggcctctca agtagctggg attacaggca   1060

tctgccacca tgcccggcaa attttttgtgt ttttagtaga gacagggttt tgccatgttg   1120

gccaggctgg tctcgaactc ctgatctcag gtgattcacc cgcctcagcc ttccaaagtg   1180

ctgggattat aggtgtgagc caccgcgccc ggcctggatc tgttttctta gcacgcagtg   1240

aggaatcttt gtacttaagg ccagggcaac aaagtcaaga ggtcaaggtg tagggccatg   1300

aggcctggac ctatgctgca ggcaagggtt tccatccccg ctgccctagg cactctcttc   1360

ccaaggccag gttgggcacc tggggaggtc agttcagaaa tatctagcag agacctctta   1420

aaccccatc ccagcacccc atcctgttgt tcccagagct ggtctcccat gagtgtgcta    1480

gagccagata gccgtggccc cccacccatc tcactcacac acacaggcat ccatacaccc   1540

cagaagactt cccaaatgag gccagactca gggtcacggg gaatgtgctt ctgcccctgt   1600

aagggctttg gggaaggggg caacatagta gaggctggaa agagccccca aacctgtgcc   1660

catgcccctc cagccctgcg tttccattct gccttctcag agtgcccttg ctgcacccag   1720

accaccggcc aggagagacc ttctctccca ctccagcccc tctcactgcc cttcaactag   1780

agctttcacc tttttacatt tcccttctga aggacacaaa tctgcttttc tgcccataca   1840

ctggcccaag ggctcaccta acttgggagg gaaggggctg ttggtacaag gatgattttc   1900

tgttagactg ccattttgca cggtctcccc cttcccatct gatgtgtcct gccctcagc    1960

tctttgcctt atctgtgtca ctgtcacttt agcaaaaata cagcggccat ttgtatc      2017
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<210> 29

<211> 1606

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (30)... (1250)

<400> 29

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acctcttccg tcggctgaat tgcggccgt atg cgc ggc tct gtg gag tgc acc        53
                                Met Arg Gly Ser Val Glu Cys Thr
                                 1               5

tgg ggt tgg ggg cac tgt gcc ccc agc ccc ctg ctc ctt tgg act cta       101
Trp Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr Leu
    10                  15                  20

ctt ctg ttt gca gcc cca ttt ggc ctg ctg ggg gag aag acc cgc cag       149
Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg Gln
25                  30                  35                  40

gtg tct ctg gag gtc atc cct aac tgg ctg ggc ccc ctg cag aac ctg       197
Val Ser Leu Glu Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu
                45                  50                  55

ctt cat ata cgg gca gtg ggc acc aat tcc aca ctg cac tat gtg tgg       245
Leu His Ile Arg Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp
                60                  65                  70

agc agc ctg ggg cct ctg gca gtg gta atg gtg gcc acc aac acc ccc       293
Ser Ser Leu Gly Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro
                75                  80                  85

cac agc acc ctg agc gtc aac tgg agc ctc ctg cta tcc cct gag ccc       341
His Ser Thr Leu Ser Val Asn Trp Ser Leu Leu Leu Ser Pro Glu Pro
    90                  95                  100
```

gat ggg ggc ctg atg gtg ctc cct aag gac agc att cag ttt tct tct   389
Asp Gly Gly Leu Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser
105   110   115   120

gcc ctt gtt ttt acc agg ctg ctt gag ttt gac agc acc aac gtg tcc   437
Ala Leu Val Phe Thr Arg Leu Leu Glu Phe Asp Ser Thr Asn Val Ser
           125   130   135

gat acg gca gca aag cct ttg gga aga cca tat cct cca tac tcc ttg   485
Asp Thr Ala Ala Lys Pro Leu Gly Arg Pro Tyr Pro Pro Tyr Ser Leu
           140   145   150

gcc gat ttc tct tgg aac aac atc act gat tca ttg gat cct gcc acc   533
Ala Asp Phe Ser Trp Asn Asn Ile Thr Asp Ser Leu Asp Pro Ala Thr
           155   160   165

ctg agt gcc aca ttt caa ggc cac ccc atg aac gac cct acc agg act   581
Leu Ser Ala Thr Phe Gln Gly His Pro Met Asn Asp Pro Thr Arg Thr
           170   175   180

ttt gcc aat ggc agc ctg gcc ttc agg gtc cag gcc ttt tcc agg tcc   629
Phe Ala Asn Gly Ser Leu Ala Phe Arg Val Gln Ala Phe Ser Arg Ser
185   190   195   200

agc cga cca gcc caa ccc cct cgc ctc ctg cac aca gca gac acc tgt   677
Ser Arg Pro Ala Gln Pro Pro Arg Leu Leu His Thr Ala Asp Thr Cys
           205   210   215

cag cta gag gtg gcc ctg att gga gcc tct ccc cgg gga aac cgt tcc   725
Gln Leu Glu Val Ala Leu Ile Gly Ala Ser Pro Arg Gly Asn Arg Ser
           220   225   230

ctg ttt ggg ctg gag gta gcc aca ttg ggc cag ggc cct gac tgc ccc   773

Leu Phe Gly Leu Glu Val Ala Thr Leu Gly Gln Gly Pro Asp Cys Pro
        235   240   245

tca atg cag gag cag cac tcc atc gac gat gaa tat gca ccg gcc gtc   821
Ser Met Gln Glu Gln His Ser Ile Asp Asp Glu Tyr Ala Pro Ala Val
        250   255   260

ttc cag ttg gac cag cta ctg tgg ggc tcc ctc cca tca ggc ttt gca   869
Phe Gln Leu Asp Gln Leu Leu Trp Gly Ser Leu Pro Ser Gly Phe Ala
265   270   275   280

cag tgg cga cca gtg gct tac tcc cag aag ccg ggg ggc cga gaa tca   917
Gln Trp Arg Pro Val Ala Tyr Ser Gln Lys Pro Gly Gly Arg Glu Ser
                285   290   295

gcc ctg ccc tgc caa gct tcc cct ctt cat cct gcc tta gca tac tct   965
Ala Leu Pro Cys Gln Ala Ser Pro Leu His Pro Ala Leu Ala Tyr Ser
                300   305   310

ctt ccc cag tca ccc att gtc cga gcc ttc ttt ggg tcc cag aat aac   1013
Leu Pro Gln Ser Pro Ile Val Arg Ala Phe Phe Gly Ser Gln Asn Asn
                315   320   325

ttc tgt gcc ttc aat ctg acg ttc ggg gct tcc aca ggc cct ggc tat   1061
Phe Cys Ala Phe Asn Leu Thr Phe Gly Ala Ser Thr Gly Pro Gly Tyr
        330   335   340

tgg gac caa cac tac ctc agc tgg tcg atg ctc ctg ggt gtg ggc ttc   1109
Trp Asp Gln His Tyr Leu Ser Trp Ser Met Leu Leu Gly Val Gly Phe
345   350   355   360

cct cca gtg gac ggc ttg tcc cca cta gtc ctg ggc atc atg gca gtg   1157
Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val

```
                        365                 370                 375
gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg        1205
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu

                  380                 385                 390
ctg ctg cac cac aag aag tac tca gag tac cag tcc ata aat taa            1250
Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn

              395                 400                 405
ggcccgctct ctggagggaa ggacattact gaacctgtct tgctgtgcct cgaaactctg      1310

gaggttggag catcaagttc cagccggccc cttcactccc ccatcttgct tttctgtgga      1370

acctcagagg ccagcctcga cttcctggag accccaggt ggggcttcct tcatactttg       1430

ttgggggact ttggaggcgg gcaggggaca gggctattga taaggtcccc ttggtgttgc      1490

cttcttgcat ctccacacat ttcccttgga tgggacttgc aggcctaaat gagaggcatt      1550

ctgactggtt ggctgccctg gaaggcaaga aaatagattt atttttttc acaggg          1606
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<210> 30

<211> 1695

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)...(631)

<400> 30

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acagccgagc agctggagcg atcgaggctg cagcgcggcc gccgggcgca gc atg        55
                                                             Met
                                                               1
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act gcc gtc ggc gtg cag gcc cag agg cct ttg ggc caa agg cag ccc     103
Thr Ala Val Gly Val Gln Ala Gln Arg Pro Leu Gly Gln Arg Gln Pro
              5                   10                  15

cgc cgg tcc ttc ttt gaa tcc ttc atc cgg acc ctc atc atc acg tgt     151
Arg Arg Ser Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr Cys
              20                  25                  30

gtg gcc ctg gct gtg gtc ctg tcc tcg gtc tcc att tgt gat ggg cac     199
Val Ala Leu Ala Val Val Leu Ser Ser Val Ser Ile Cys Asp Gly His
              35                  40                  45

tgg ctc ctg gct gag gac cgc ctc ttc ggg ctc tgg cac ttc tgc acc     247
Trp Leu Leu Ala Glu Asp Arg Leu Phe Gly Leu Trp His Phe Cys Thr
    50                  55                  60                  65

acc acc aac cag agt gtg ccg atc tgc ttc aga gac ctg ggc cag gcc     295
Thr Thr Asn Gln Ser Val Pro Ile Cys Phe Arg Asp Leu Gly Gln Ala
              70                  75                  80

cat gtg ccc ggg ctg gcc gtg ggc atg ggc ctg gta cgc agc gtg ggc     343
His Val Pro Gly Leu Ala Val Gly Met Gly Leu Val Arg Ser Val Gly
              85                  90                  95

gcc ttg gcc gtg gtg gcc gcc att ttt ggc ctg gag ttc ctc atg gtg     391
Ala Leu Ala Val Val Ala Ala Ile Phe Gly Leu Glu Phe Leu Met Val
              100                 105                 110

tcc cag ttg tgc gag gac aaa cac tca cag tgc aag tgg gtc atg ggt     439
Ser Gln Leu Cys Glu Asp Lys His Ser Gln Cys Lys Trp Val Met Gly
              115                 120                 125

tcc atc ctc ctc ctg gtg tct ttc gtc ctc tcc tcc ggc ggg ctc ctg     487
```

```
            Ser Ile Leu Leu Leu Val Ser Phe Val Leu Ser Ser Gly Gly Leu Leu
            130             135             140             145

ggt ttt gtg atc ctc ctc agg aac caa gtc aca ctc atc ggc ttc acc        535
Gly Phe Val Ile Leu Leu Arg Asn Gln Val Thr Leu Ile Gly Phe Thr
                150             155             160

cta atg ttt tgg tgc gaa ttc act gcc tcc ttc ctc ctc ttc ctg aac        583
Leu Met Phe Trp Cys Glu Phe Thr Ala Ser Phe Leu Leu Phe Leu Asn
                165             170             175

gcc atc agc ggc ctt cac atc aac agc atc acc cat ccc tgg gaa tg         630
Ala Ile Ser Gly Leu His Ile Asn Ser Ile Thr His Pro Trp Glu
                180             185             190

accgtggaaa ttttaggccc cctccaggga catcagattc cacaagaaaa tatggtcaaa      690

atgggacttt tccagcatgt ggcctctggt ggggctgggt tggacaaggg ccttgaaacg      750

gctgcctgtt tgccgataac ttgtgggtgg tcagccagaa atggcccggg ggcctctgca      810

cctggtctgc agggccagag gccaggaggg tgcctcagtg ccaccaactg cacaggctta      870

gccagatgtt gattttagag gaagaaaaaa acattttaaa actccttctt gaattttctt      930

ccctggactg gaatacagtt ggaagcacag gggtaactgg tacctgagct agctgcacag      990

ccaaggatag ttcatgcctg tttcattgac acgtgctggg atagggggctg cagaatccct     1050

ggggctccca gggttgttaa gaatggatca ttcttccagc taagggtcca atcagtgcct      1110

attcttccac cagctcaaag ggccttcgta tgtatgtccc tggcttcagc tttggtcatg      1170

ccaaagaggc agagttcagg attccctcag aatgccctgc acacagtagg tttccaaacc      1230

atttgactcg gtttgcctcc ctgcccgttg tttaaacctt acaaaccctg gataacccca      1290

tcttctagca gctggctgtc ccctctggga gctctgccta tcagaaccct accttaaggt      1350

gggtttcctt ccgagaagag ttcttgagca agctctccca ggagggccca cctgactgct      1410

aatacacagc cctccccaag gcccgtgtgt gcatgtgtct gtcttttgtg agggttagac      1470
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agcctcaggg caccattttt aatcccagaa cacatttcaa agagcacgta tctagacctg   1530

ctggactctg caggggggtga gggggaacag cgagagcttg ggtaatgatt aacacccatg   1590

ctggggatgc atggaggtga aggggggccag gaaccagtgg agatttccat ccttgccagc   1650

acgtctgtac ttctgttcat taaagtgctc cctttctagt ccttt   1695

<210> 31

<211> 377

<212> PRT

<213> Homo sapiens

<400> 31

Met Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly

 1   5   10   15

Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile

            20   25   30

Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe

            35   40   45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser

        50   55   60

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile

    65   70   75   80

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe

                85   90   95

Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu

            100   105   110

Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe

                    115   120   125

Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln

        130   135   140

Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr

145   150   155   160

Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr

                165   170   175

Leu Leu Arg Lys His Trp Ile Ala Asn Asn Leu Phe Gly Leu Ala Phe

                    180   185   190

Ser Leu Asn Gly Val Glu Leu Leu His Leu Asn Asn Val Ser Thr Gly

                195   200   205

Cys Ile Leu Leu Gly Gly Leu Phe Ile Tyr Asp Val Phe Trp Val Phe

        210   215   220

Gly Thr Asn Val Met Val Thr Val Ala Lys Ser Phe Glu Ala Pro Ile

225   230   235   240

Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn

                245   250   255

Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val Ile Pro Gly Ile Phe

                260   265   270

Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu Lys Lys Asn Thr His

                275   280   285

Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu

        290   295   300

Thr Ile Phe Ile Met His Ile Phe Lys His Ala Gln Pro Ala Leu Leu

305   310   315   320

Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val Leu Val Ala Leu Ala
              325   330   335

Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys
              340   345   350

Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala
              355   360   365

Ser Lys Gly Leu Glu Lys Lys Glu Lys
        370   375

<210> 32

<211> 81

<212> PRT

<213> Homo sapiens

<400> 32

Met Thr Ala His Ser Phe Ala Leu Pro Val Ile Ile Phe Thr Thr Phe
     1   5   10   15

Trp Gly Leu Val Gly Ile Ala Gly Pro Trp Phe Val Pro Lys Gly Pro
              20   25   30

Asn Arg Gly Val Ile Ile Thr Met Leu Val Ala Thr Ala Val Cys Cys
           35   40   45

Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu Phe
        50   55   60

Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Val Arg Phe Leu Trp
     65   70   75   80

Glu

<210> 33

<211> 487

<212> PRT

<213> Homo sapiens

<400> 33

Met Gly Asp Thr Gly Leu Arg Lys Arg Arg Glu Asp Glu Lys Ser Ile
1   5   10   15

Gln Ser Gln Glu Pro Lys Thr Thr Ser Leu Gln Lys Glu Leu Gly Leu
                20   25   30

Ile Ser Gly Ile Ser Ile Ile Val Gly Thr Ile Ile Gly Ser Gly Ile
            35   40   45

Phe Val Ser Pro Lys Ser Val Leu Ser Asn Thr Glu Ala Val Gly Pro
        50   55   60

Cys Leu Ile Ile Trp Ala Ala Cys Gly Val Leu Ala Thr Leu Gly Ala
65   70   75   80

Leu Cys Phe Ala Glu Leu Gly Thr Met Ile Thr Lys Ser Gly Gly Glu
                85   90   95

Tyr Pro Tyr Leu Met Glu Ala Tyr Gly Pro Ile Pro Ala Tyr Leu Phe
                100   105   110

Ser Trp Ala Ser Leu Ile Val Ile Lys Pro Thr Ser Phe Ala Ile Ile
            115   120   125

Cys Leu Ser Phe Ser Glu Tyr Val Cys Ala Pro Phe Tyr Val Gly Cys
        130   135   140

Lys Pro Pro Gln Ile Val Val Lys Cys Leu Ala Ala Ala Ala Ile Leu
145   150   155   160

Phe Ile Ser Thr Val Asn Ser Leu Ser Val Arg Leu Gly Ser Tyr Val
                165   170   175

Gln Asn Ile Phe Thr Ala Ala Lys Leu Val Ile Val Ala Ile Ile Ile
            180   185   190

Ile Ser Gly Leu Val Leu Leu Ala Gln Gly Asn Thr Lys Asn Phe Asp
            195   200   205

Asn Ser Phe Glu Gly Ala Gln Leu Ser Val Gly Ala Ile Ser Leu Ala
        210   215   220

Phe Tyr Asn Gly Leu Trp Ala Tyr Asp Gly Trp Asn Gln Leu Asn Tyr
225   230   235   240

Ile Thr Glu Glu Leu Arg Asn Pro Tyr Arg Asn Leu Pro Leu Ala Ile
                245   250   255

Ile Ile Gly Ile Pro Leu Val Thr Ala Cys Tyr Ile Leu Met Asn Val
            260   265   270

Ser Tyr Phe Thr Val Met Thr Ala Thr Glu Leu Leu Gln Ser Gln Ala
            275   280   285

Val Ala Val Thr Phe Gly Asp Arg Val Leu Tyr Pro Ala Ser Trp Ile
        290   295   300

Val Pro Leu Phe Val Ala Phe Ser Thr Ile Gly Ala Ala Asn Gly Thr
305   310   315   320

Cys Phe Thr Ala Gly Arg Leu Ile Tyr Val Ala Gly Arg Glu Gly His
            325   330   335

Met Leu Lys Val Leu Ser Tyr Ile Ser Val Arg Arg Leu Thr Pro Ala

```
                340               345               350
Pro Ala Ile Ile Phe Tyr Gly Ile Ile Ala Thr Ile Tyr Ile Ile Pro
        355               360               365
Gly Asp Ile Asn Ser Leu Val Asn Tyr Phe Ser Phe Ala Ala Trp Leu
        370               375               380
Phe Tyr Gly Leu Thr Ile Leu Gly Leu Ile Val Met Arg Phe Thr Arg
385               390               395               400
Lys Glu Leu Glu Arg Pro Ile Lys Val Pro Val Val Ile Pro Val Leu
                405               410               415
Met Thr Leu Ile Ser Val Phe Leu Val Leu Ala Pro Ile Ile Ser Lys
                420               425               430
Pro Thr Trp Glu Tyr Leu Tyr Cys Val Leu Phe Ile Leu Ser Gly Leu
        435               440               445
Leu Phe Tyr Phe Leu Phe Val His Tyr Lys Phe Gly Trp Ala Gln Lys
        450               455               460
Ile Ser Lys Pro Ile Thr Met His Leu Gln Met Leu Met Glu Val Val
465               470               475               480
Pro Pro Glu Glu Asp Pro Glu
                485
```

<210> 34

<211> 375

<212> PRT

<213> Homo sapiens

<400> 34

```
Met Thr Pro Gln Pro Ala Gly Pro Pro Asp Gly Gly Trp Gly Trp Val
 1               5                  10                 15

Val Ala Ala Ala Ala Phe Ala Ile Asn Gly Leu Ser Tyr Gly Leu Leu
            20                  25                 30

Arg Ser Leu Gly Leu Ala Phe Pro Asp Leu Ala Glu His Phe Asp Arg
            35                  40                 45

Ser Ala Gln Asp Thr Ala Trp Ile Ser Ala Leu Ala Leu Ala Val Gln
        50                  55                 60

Gln Ala Ala Ser Pro Val Gly Ser Ala Leu Ser Thr Arg Trp Gly Ala
 65                 70                  75                 80

Arg Pro Val Val Met Val Gly Gly Val Leu Ala Ser Leu Gly Phe Val
                85                  90                 95

Phe Ser Ala Phe Ala Ser Gly Leu Leu His Leu Tyr Leu Gly Leu Gly
            100                 105                110

Leu Leu Ala Gly Phe Gly Trp Ala Leu Val Phe Ala Pro Ala Leu Gly
            115                 120                125

Thr Leu Ser Arg Tyr Phe Ser Arg Arg Arg Val Leu Ala Val Gly Leu
        130                 135                140

Ala Leu Thr Gly Asn Gly Ala Ser Ser Leu Leu Leu Ala Pro Ala Leu
145                 150                 155                160

Gln Leu Leu Leu Asp Thr Phe Gly Trp Arg Gly Ala Leu Leu Leu Leu
            165                 170                175

Gly Ala Ile Thr Leu His Leu Thr Pro Cys Gly Ala Leu Leu Leu Pro
            180                 185                190

Leu Val Leu Pro Gly Asp Pro Pro Ala Pro Pro Arg Ser Pro Leu Ala
```

```
                 195                    200                    205
Ala Leu Gly Leu Ser Leu Phe Thr Arg Arg Ala Phe Ser Ile Phe Ala

        210                    215                   220
Leu Gly Thr Ala Leu Val Gly Gly Gly Tyr Phe Val Pro Tyr Val His

225                    230                    235                    240
Leu Ala Pro Arg Phe Arg Pro Gly Pro Gly Gly Ile Arg Ser Ser Ala

                245                    250                    255
Gly Gly Gly Arg Gly Cys Asp Gly Gly Cys Gly Arg Pro Ala Gly Leu

                260                    265                    270
Arg Val Ala Gly Arg Pro Arg Leu Gly Ala Pro Pro Ala Ala Ala Gly

        275                    280                    285
Arg Ile Arg Gly Ser Asp Trp Ala Gly Ala Val Gly Gly Gly Ala Gly

        290                    295                    300
Ala Arg Gly Gly Arg Arg Arg Glu Leu Gly Gly Ser Pro Ala Gly Arg

305                    310                    315                    320
Gly Cys Gly Leu Trp Ala Glu Arg Gly Glu Leu Arg Pro Ala Gly Phe

                325                    330                    335
Arg Cys Thr Pro Arg Ala Gly Gly Arg Arg Arg Cys Gly Ala Gly His

        340                    345                    350
Arg Ala Gly Asp Asp Ala Asp Glu Pro Arg Gly Ala Pro Gly Pro Ser

        355                    360                    365
Pro Val Arg Leu Pro Lys Gly

        370                    375
```

<210> 35

<211> 350

<212> PRT

<213> Homo sapiens

<400> 35

Met Ala Thr Thr Ala Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly
1   5   10   15

Pro Glu Trp Gly Gly Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala
                20   25   30

Val Ile Asp Met Glu Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu
            35   40   45

Asp Met Gly Glu Leu His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala
        50   55   60

Asp Ala Ala Asp Ala Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu
65   70   75   80

Gly Met Lys Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln
                85   90   95

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr
                100   105   110

Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln
                115   120   125

Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn
                130   135   140

Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val
145   150   155   160

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr

```
                165                  170                  175
Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe
                180                  185                  190
Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu
                195                  200                  205
Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr
            210                  215                  220
Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His
    225                  230                  235                  240
Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser
                245                  250                  255
Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr
                260                  265                  270
Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe
            275                  280                  285
Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu
        290                  295                  300
Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg
    305                  310                  315                  320
Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu
                325                  330                  335
Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His
            340                  345                  350
```

<210> 36

<211> 667

<212> PRT

<213> Homo sapiens

<400> 36

Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr Glu
1   5   10   15

Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly Glu
            20   25   30

Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Pro
            35   40   45

Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu
            50   55   60

Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp Cys
65   70   75   80

Val Arg Gly Arg Pro Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly
                85   90   95

Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe Met Val Leu Leu Ser
            100   105   110

Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala Leu Pro Phe Leu Thr
            115   120   125

Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr Glu Ala Pro Arg Gly
            130   135   140

Ala Trp Lys Ile Leu Gly Leu Phe Tyr Tyr Ala Ala Leu Tyr Tyr Pro
145   150   155   160

Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala Ala His Leu Leu Gly

```
              165               170               175
Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln Val Trp Gln Arg Ala

          180               185               190
Glu Cys Pro Gln Val Pro Lys Ile Tyr Lys Tyr Tyr Ser Leu Leu Ala

          195               200               205
Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu Ser Leu Trp Tyr Pro

      210               215               220
Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr Gly Ala Gly Ser Lys

  225               230               235               240
Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu Arg Asn Leu Leu Cys

              245               250               255
Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser Lys His Gly Phe Leu

          260               265               270
Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile Tyr Thr Pro Gln Pro

          275               280               285
Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser Ala Thr Leu Thr Gly

          290               295               300
Thr Ala Ile Tyr Gln Val Ala Leu Leu Leu Leu Val Gly Val Val Pro

  305               310               315               320
Thr Ile Gln Lys Val Arg Ala Gly Val Thr Thr Asp Val Ser Tyr Leu

          325               330               335
Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp Lys Gln Glu Val Val

          340               345               350
Glu Leu Val Lys His His Leu Trp Ala Leu Glu Val Cys Tyr Ile Ser

      355               360               365
```

Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu Val Leu Met Arg Ser
        370   375   380

Leu Val Thr His Arg Thr Asn Leu Arg Ala Leu His Arg Gly Ala Ala
385   390   395   400

Leu Asp Leu Ser Pro Leu His Arg Ser Pro His Pro Ser Arg Gln Ala
                405   410   415

Ile Phe Cys Trp Met Ser Phe Ser Ala Tyr Gln Thr Ala Phe Ile Cys
                420   425   430

Leu Gly Leu Leu Val Gln Gln Ile Ile Phe Phe Leu Gly Thr Thr Ala
                435   440   445

Leu Ala Phe Leu Val Leu Met Pro Val Leu His Gly Arg Asn Leu Leu
        450   455   460

Leu Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe Trp Leu Thr Leu Ala
465   470   475   480

Leu Ala Val Ile Leu Gln Asn Met Ala Ala His Trp Val Phe Leu Glu
                485   490   495

Thr His Asp Gly His Pro Gln Leu Thr Asn Arg Arg Val Leu Tyr Ala
                500   505   510

Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu Val Gly Ala Met Val
                515   520   525

Ala Thr Trp Arg Val Leu Leu Ser Ala Leu Tyr Asn Ala Ile His Leu
        530   535   540

Gly Gln Met Asp Leu Ser Leu Leu Pro Pro Arg Ala Ala Thr Leu Asp
545   550   555   560

Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys Ile Glu Val Ser Gln

```
              565               570               575
Ser His Pro Ala Met Thr Ala Phe Cys Ser Leu Leu Leu Gln Ala Gln
              580               585               590
Ser Leu Leu Pro Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro
              595               600               605
Gly Glu Glu Asp Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Ser Met
          610               615               620
Ala Lys Gly Ala Arg Pro Gly Ala Ser Arg Gly Arg Ala Arg Trp Gly
    625               630               635               640
Leu Ala Tyr Thr Leu Leu His Asn Pro Thr Leu Gln Val Phe Arg Lys
              645               650               655
Thr Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro
              660               665
```

<210> 37

<211> 464

<212> PRT

<213> Homo sapiens

<400> 37

```
Met Ile Val Cys Leu Leu Phe Met Met Ile Leu Leu Ala Lys Glu Val
    1               5                10               15
Gln Leu Val Asp Gln Thr Asp Ser Pro Leu Leu Ser Leu Leu Gly Gln
              20               25               30
Thr Ser Ser Leu Ser Trp His Leu Val Asp Ile Val Ser Tyr Gln Ser
          35               40               45
```

Val Leu Ser Tyr Phe Ser Ser His Tyr Pro Pro Ser Ile Ile Leu Ala
      50   55   60

Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys Leu Leu Lys Val Ser Ala
65   70   75   80

Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys His Leu Asp Ala Val Pro
               85   90   95

Lys Cys Gln Ala Phe Thr His Gln Met Val Gln Phe Leu Ser Thr Leu
          100   105   110

Glu Gln Asn Gly Lys Ile Thr Leu Ala Val Leu Glu Gln Glu Met Ser
          115   120   125

Lys Leu Leu Asp Asp Ile Ile Val Phe Asn Pro Pro Asp Met Asp Ser
          130   135   140

Gln Thr Arg His Met Ala Leu Ser Ser Leu Phe Met Glu Val Leu Met
145   150   155   160

Met Met Asn Asn Ala Thr Ile Pro Thr Ala Glu Phe Leu Arg Gly Ser
               165   170   175

Ile Arg Thr Trp Ile Gly Gln Lys Met His Gly Leu Val Val Leu Pro
          180   185   190

Leu Leu Thr Ala Ala Cys Gln Ser Leu Ala Ser Val Arg His Met Ala
          195   200   205

Glu Thr Thr Glu Ala Cys Ile Thr Ala Tyr Phe Lys Glu Ser Pro Leu
          210   215   220

Asn Gln Asn Ser Gly Trp Gly Pro Ile Leu Val Ser Leu Gln Val Pro
225   230   235   240

Glu Leu Thr Met Glu Glu Phe Leu Gln Glu Cys Leu Thr Leu Gly Ser

```
              245                 250                 255
Tyr Leu Thr Leu Tyr Val Tyr Leu Leu Gln Cys Leu Asn Ser Glu Gln

              260                 265                 270
Thr Leu Arg Asn Glu Met Lys Val Leu Leu Ile Leu Ser Lys Trp Leu

              275                 280                 285
Glu Gln Val Tyr Pro Ser Ser Val Glu Glu Glu Ala Lys Leu Phe Leu

              290                 295                 300
Trp Trp His Gln Val Leu Gln Leu Ser Leu Ile Gln Thr Glu Gln Asn

305                 310                 315                 320
Asp Ser Val Leu Thr Glu Ser Val Ile Arg Ile Leu Leu Leu Val Gln

              325                 330                 335
Ser Arg Gln Asn Leu Val Ala Glu Glu Arg Leu Ser Ser Gly Ile Leu

              340                 345                 350
Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro Leu Ser Asn Arg Phe Arg

              355                 360                 365
Val Val Ala Arg Ser Met Ala Ala Phe Leu Ser Val Gln Val Pro Met

              370                 375                 380
Glu Asp Gln Ile Arg Leu Arg Pro Gly Ser Glu Leu His Leu Thr Pro

385                 390                 395                 400
Lys Ala Gln Gln Ala Leu Asn Ala Leu Glu Ser Met Ala Ser Ser Lys

              405                 410                 415
Gln Tyr Val Glu Tyr Gln Asp Gln Ile Leu Gln Ala Thr Gln Phe Ile

              420                 425                 430
Arg His Pro Gly His Cys Leu Gln Asp Gly Lys Ser Phe Leu Ala Leu

              435                 440                 445
```

Leu Val Asn Cys Leu Tyr Pro Glu Val His Tyr Leu Asp His Ile Arg

    450   455   460

<210> 38

<211> 470

<212> PRT

<213> Homo sapiens

<400> 38

Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu

 1   5   10   15

Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser

              20   25   30

Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro

              35   40   45

Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met

    50   55   60

Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro

65   70   75   80

Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe

                  85   90   95

Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg

                  100   105   110

Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys

              115   120   125

His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe

```
            130                 135                 140
Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr
145                 150                 155                 160
Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr
                165                 170                 175
Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu
                    180                 185                 190
Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly
                    195                 200                 205
Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser
                210                 215                 220
Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro
225                 230                 235                 240
Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys
                    245                 250                 255
Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser
                    260                 265                 270
Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys
                    275                 280                 285
Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly
                290                 295                 300
Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp
305                 310                 315                 320
Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu
                    325                 330                 335
```

Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val

340 345 350

Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu

355 360 365

Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys

370 375 380

Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu

385 390 395 400

Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe

405 410 415

Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly

420 425 430

Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro

435 440 445

Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu

450 455 460

Glu Val Ile Leu Arg Asp

465 470

<210> 39

<211> 243

<212> PRT

<213> Homo sapiens

<400> 39

Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro Val Asn Val Phe

```
         1                5                10               15
Ser Val Thr Pro Tyr Thr Pro Ser Thr Ala Asp Ile Gln Val Ser Asp

                 20               25               30
Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly Ile Phe Leu Gly

                 35               40               45
Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile Lys Tyr Gln Gly

          50               55               60
Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro Val Leu Leu Ser

     65               70               75               80
Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys Phe Lys Met Leu

                 85               90               95
Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val Pro Asp Ser Glu

                 100              105              110
Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly Ile Asn Gln Pro

                 115              120              125
Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile Pro Pro Pro Tyr

                 130              135              140
Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr Leu Gln Ser Val

     145              150              155              160
Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala Ala Ala Ala Met

                 165              170              175
Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln Asp Asn Ser Ala

                 180              185              190
Phe Val Val Asp Glu Gly Cys Leu Ser Phe Thr Asp Gly Gly Asn His

          195              200              205
```

Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr Gln Leu Glu Glu
        210   215   220

Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu Glu Ile Tyr Ser
225   230   235   240

Leu Pro Arg

<210> 40

<211> 270

<212> PRT

<213> Homo sapiens

<400> 40

Met Ala Gly Ala Glu Asp Trp Pro Gly Gln Gln Leu Glu Leu Asp Glu
    1   5   10   15

Asp Glu Ala Ser Cys Cys Arg Trp Gly Ala Gln His Ala Gly Ala Arg
                20   25   30

Glu Leu Ala Ala Leu Tyr Ser Pro Gly Lys Arg Leu Gln Glu Trp Cys
            35   40   45

Ser Val Ile Leu Cys Phe Ser Leu Ile Ala His Asn Leu Val His Leu
        50   55   60

Leu Leu Leu Ala Arg Trp Glu Asp Thr Pro Leu Val Ile Leu Gly Val
65   70   75   80

Val Ala Gly Ala Leu Ile Ala Asp Phe Leu Ser Gly Leu Val His Trp
                85   90   95

Gly Ala Asp Thr Trp Gly Ser Val Glu Leu Pro Ile Val Gly Lys Ala
            100   105   110

Phe Ile Arg Pro Phe Arg Glu His His Ile Asp Pro Thr Ala Ile Thr
        115   120   125

Arg His Asp Phe Ile Glu Thr Asn Gly Asp Asn Cys Leu Val Thr Leu
        130   135   140

Leu Pro Leu Leu Asn Met Ala Tyr Lys Phe Arg Thr His Ser Pro Glu
145   150   155   160

Ala Leu Glu Gln Leu Tyr Pro Trp Glu Cys Phe Val Phe Cys Leu Ile
                165   170   175

Ile Phe Gly Thr Phe Thr Asn Gln Ile His Lys Trp Ser His Thr Tyr
                180   185   190

Phe Gly Leu Pro Arg Trp Val Thr Leu Leu Gln Asp Trp His Val Ile
                195   200   205

Leu Pro Arg Lys His His Arg Ile His His Val Ser Pro His Glu Thr
        210   215   220

Tyr Phe Cys Ile Thr Thr Gly Trp Leu Asn Tyr Pro Leu Glu Lys Ile
225   230   235   240

Gly Phe Trp Arg Arg Leu Glu Asp Leu Ile Gln Gly Leu Thr Gly Glu
                245   250   255

Lys Pro Arg Ala Asp Asp Met Lys Trp Ala Gln Lys Ile Lys
        260   265   270

<210> 41

<211> 1131

<212> DNA

<213> Homo sapiens

<400> 41

atggactcgg	ccctcagcga	tccgcataac	ggcagtgccg	aggcaggcgg	ccccaccaac	60
agcactacgc	ggccgccttc	cacgcccgag	ggcatcgcgc	tggcctacgg	cagcctcctg	120
ctcatggcgc	tgctgcccat	cttcttcggc	gccctgcgct	ccgtacgctg	cgcccgcggc	180
aagaatgctt	cagacatgcc	tgaaacaatc	accagccggg	atgccgcccg	cttccccatc	240
atcgccagct	gcacactctt	ggggctctac	ctcttttca	aaatattctc	ccaggagtac	300
atcaacctcc	tgctgtccat	gtatttcttc	gtgctgggaa	tcctggccct	gtcccacacc	360
atcagcccct	tcatgaataa	gttttttcca	gccagctttc	caaatcgaca	gtaccagctg	420
ctcttcacac	agggttctgg	ggaaaacaag	gaagagatca	tcaattatga	atttgacacc	480
aaggacctgg	tgtgcctggg	cctgagcagc	atcgttggcg	tctggtacct	gctgaggaag	540
cactggattg	ccaacaacct	ttttggcctg	gccttctccc	ttaatggagt	agagctcctg	600
cacctcaaca	atgtcagcac	tggctgcatc	ctgctgggcg	gactcttcat	ctacgatgtc	660
ttctgggtat	ttggcaccaa	tgtgatggtg	acagtggcca	agtccttcga	ggcaccaata	720
aaattggtgt	ttccccagga	tctgctggag	aaaggcctcg	aagcaaacaa	ctttgccatg	780
ctgggacttg	gagatgtcgt	cattccaggg	atcttcattg	ccttgctgct	gcgctttgac	840
atcagcttga	agaagaatac	ccacacctac	ttctacacca	gctttgcagc	ctacatcttc	900
ggcctgggcc	ttaccatctt	catcatgcac	atcttcaagc	atgctcagcc	tgccctccta	960
tacctggtcc	ccgcctgcat	cggttttcct	gtcctggtgg	cgctggccaa	gggagaagtg	1020
acagagatgt	tcagttatga	ggagtcaaat	cctaaggatc	cagcggcagt	gacagaatcc	1080
aaagagggaa	cagaggcatc	agcatcgaag	gggctggaga	agaaagagaa	a	1131

<210> 42

<211> 243

<212> DNA

<213> Homo sapiens

<400> 42

```
atgacggcgc actcattcgc cctcccggtc atcatcttca ccacgttctg gggcctcgtc        60

ggcatcgccg ggccctggtt cgtgccgaag ggacccaacc gcggagtgat catcaccatg       120

ctggtcgcca ccgccgtctg ctgttacctc ttctggctca tcgccatcct ggcgcagctg       180

aacccccctgt tcgggcccca gctgaagaat gagaccatct ggtacgtgcg cttcctgtgg       240

gag                                                                     243
```

<210> 43

<211> 1461

<212> DNA

<213> Homo sapiens

<400> 43

```
atgggggata ctggcctgag aaagcggaga gaggatgaga agtcgatcca gagccaagag        60

cctaagacca ccagtctcca aaaggagctg ggcctcatca gtggcatctc catcatcgtg       120

ggcaccatca ttggctctgg gatcttcgtt tcccccaagt ctgtgctcag caacacggaa       180

gctgtggggc cctgcctcat catatgggcg gcttgcgggg tcctcgcgac gctgggtgcc       240

ctgtgctttg cggagcttgg cacaatgatc accaagtcag ggggagagta tccctacctg       300

atggaggcct acgggcccat ccccgcctac ctcttctcct gggccagcct gatcgtcatt       360

aagcccacgt ccttcgccat catctgcctc agcttctccg agtatgtgtg tgcgcccttc       420

tatgtgggct gcaagcctcc tcaaatcgtt gtgaaatgcc tggccgccgc cgccatcttg       480

ttcatctcga cagtgaactc actgagcgtg cggctgggaa gctacgtcca gaacatcttc       540

accgcggcca agctggtgat cgtggccatc atcatcatca gcgggctggt gctcctggcc       600

caaggaaaca caaagaattt tgataattct ttcgagggcg cccagctgtc tgtgggagcc       660

atcagcctgg cgttttacaa tggactctgg gcctatgatg gatggaatca actcaattac       720

atcacagaag aacttagaaa cccttacaga aacctgcctt tggccattat catcgggatc       780
```

```
cccctggtga cggcgtgcta catcctcatg aacgtgtcct acttcaccgt gatgactgcc   840

accgaactcc tgcagtccca ggcggtggct gtgacatttg gtgaccgtgt tctctatcct   900

gcttcttgga tcgttccact ttttgtggca ttttcaacca tcggtgctgc taacgggacc   960

tgcttcacag cgggcagact catttacgtg gcgggccggg agggtcacat gctcaaagtg   1020

ctttcttaca tcagcgtcag gcgcctcact ccagcccccg ccatcatctt ttatggtatc   1080

atagcaacga tttatatcat ccctggtgac ataaactcgt tagtcaatta tttcagcttt   1140

gccgcatggc tgttttatgg cctgacgatt ctaggactca tcgtgatgag atttacaagg   1200

aaagagctgg aaaggcctat caaggtgccc gtagtcattc ccgtcttgat gacactcatc   1260

tctgtgtttt tggttctggc tccaatcatc agcaagccca cctgggagta cctctactgt   1320

gtgctgttta tattaagcgg cctttattt tacttcctgt ttgtccacta caagtttgga   1380

tgggctcaga aaatctcaaa gccgattacc atgcaccttc agatgctaat ggaagtggtc   1440

ccaccggagg aagaccctga g                                            1461
```

<210> 44

<211> 1125

<212> DNA

<213> Homo sapiens

<400> 44

```
atgacccccc agcccgccgg acccccggat gggggctggg gctgggtggt ggcggccgca   60

gccttcgcga taaacgggct gtcctacggg ctgctgcgct cgctgggcct tgccttccct   120

gaccttgccg agcactttga ccgaagcgcc caggacactg cgtggatcag cgccctggcc   180

ctggccgtgc agcaggcagc cagccccgtg ggcagcgccc tgagcacgcg ctgggggggcc   240

cgccccgtgg tgatggttgg gggcgtcctc gcctcgctgg gcttcgtctt ctcggctttc   300

gccagcggtc tgctgcatct ctacctcggc ctgggcctcc tcgctggctt tggttgggcc   360

ctggtgttcg cccccgccct aggcaccctc tcgcgttact tctcccgccg tcgagtcttg   420
```

```
gcggtggggc  tggcgctcac  cggcaacggg  gcctcctcgc  tgctcctggc  gcccgccttg        480

cagcttctcc  tcgatacttt  cggctggcgg  ggcgctctgc  tcctcctcgg  cgcgatcacc        540

ctccacctca  ccccctgtgg  cgccctgctg  ctacccctgg  tccttcctgg  agaccccca        600

gccccaccgc  gtagtcccct  agctgccctc  ggcctgagtc  tgttcacacg  ccgggccttc        660

tcaatctttg  ctctaggcac  agccctggtt  ggggcgggt   acttcgttcc  ttacgtgcac        720

ttggctcccc  gctttagacc  ggggcctggg  gggatacgga  gcagcgctgg  tggtggccgt        780

ggctgcgatg  ggggatgcgg  gcgcccggct  ggtctgcggg  tggctggcag  accaaggctg        840

ggtgcccctc  ccgcggctgc  tggccgtatt  cggggctctg  actgggctgg  ggctgtgggt        900

ggtggggctg  gtgcccgtgg  tgggcggcga  agagagctgg  ggggtcccc   tgctggccgc        960

ggctgtggcc  tatgggctga  gcgcggggag  ttacgccccg  ctggttttcg  gtgtactccc       1020

cgggctggtg  ggcgtcggag  gtgtggtgca  ggccacaggg  ctggtgatga  tgctgatgag       1080

cctcggggggg ctcctgggcc  ctcccctgtc  aggcttccta  aggga                       1125
```

<210> 45

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 45

```
atggcaacta  cagcggcgcc  ggcgggcggc  gcccgaaatg  gagctggccc  ggaatgggga         60

gggttcgaag  aaaacatcca  gggcggaggc  tcagctgtga  ttgacatgga  gaacatggat        120

gatacctcag  gctctagctt  cgaggatatg  ggtgagctgc  atcagcgcct  gcgcgaggaa        180

gaagtagacg  ctgatgcagc  tgatgcagct  gctgctgaag  aggaggatgg  agagttcctg        240

ggcatgaagg  gctttaaggg  acagctgagc  cggcaggtgg  cagatcagat  gtggcaggct        300

gggaaaagac  aagcctccag  ggccttcagc  ttgtacgcca  acatcgacat  cctcagaccc        360

tactttgatg  tggagcctgc  tcaggtgcga  agcaggctcc  tggagtccat  gatccctatc        420
```

```
aagatggtca acttccccca gaaaattgca ggtgaactct atggacctct catgctggtc        480

ttcactctgg ttgctatcct actccatggg atgaagacgt ctgacactat tatccgggag        540

ggcaccctga tgggcacagc cattggcacc tgcttcggct actggctggg agtctcatcc        600

ttcatttact tccttgccta cctgtgcaac gcccagatca ccatgctgca gatgttggca        660

ctgctgggct atggcctctt tgggcattgc attgtcctgt tcatcaccta taatatccac        720

ctccacgccc tcttctacct cttctggctg ttggtgggtg gactgtccac actgcgcatg        780

gtagcagtgt tggtgtctcg gaccgtgggc cccacacagc ggctgctcct ctgtggcacc        840

ctggctgccc tacacatgct cttcctgctc tatctgcatt ttgcctacca caaagtggta        900

gaggggatcc tggacacact ggagggcccc aacatcccgc ccatccagag ggtccccaga        960

gacatccctg ccatgctccc tgctgctcgg cttcccacca ccgtcctcaa cgccacagcc       1020

aaagctgttg cggtgaccct gcagtcacac                                        1050



<210> 46

<211> 2001

<212> DNA

<213> Homo sapiens

<400> 46

atgtcgtccc agccagcagg gaaccagacc tcccccgggg ccacagagga ctactcctat         60

ggcagctggt acatcgatga gccccagggg ggcgaggagc tccagccaga ggggaagtg        120

ccctcctgcc acaccagcat accacccggc ctgtaccacg cctgcctggc ctcgctgtca       180

atccttgtgc tgctgctcct ggccatgctg gtgaggcgcc gccagctctg gcctgactgt       240

gtgcgtggca ggcccggcct gcccagccct gtggatttct ggctggggga caggccccgg       300

gcagtgcctg ctgctgtttt catggtcctc ttgagctccc tgtgtttgct gctccccgac       360

gaggacgcat tgcccttcct gactctcgcc tcagcaccca gccaagatgg gaaaactgag       420

gctccaagag gggcctggaa gatactggga ctgttctatt atgctgccct ctactaccct       480
```

```
ctggctgcct gtgccacggc tggccacaca gctgcacacc tgctcggcag cacgctgtcc    540

tgggcccacc ttggggtcca ggtctggcag agggcagagt gtccccaggt gcccaagatc    600

tacaagtact actccctgct ggcctccctg cctctcctgc tgggcctcgg attcctgagc    660

ctttggtacc ctgtgcagct ggtgagaagc ttcagccgta ggacaggagc aggctccaag    720

gggctgcaga gcagctactc tgaggaatat ctgaggaacc tcctttgcag gaagaagctg    780

ggaagcagct accacacctc caagcatggc ttcctgtcct gggcccgcgt ctgcttgaga    840

cactgcatct acactccaca gccaggattc catctcccgc tgaagctggt gctttcagct    900

acactgacag ggacggccat ttaccaggtg gccctgctgc tgctggtggg cgtggtaccc    960

actatccaga aggtgagggc aggggtcacc acggatgtct cctacctgct ggccggcttt   1020

ggaatcgtgc tctccgagga caagcaggag gtggtggagc tggtgaagca ccatctgtgg   1080

gctctggaag tgtgctacat ctcagccttg gtcttgtcct gcttactcac cttcctggtc   1140

ctgatgcgct cactggtgac acacaggacc aaccttcgag ctctgcaccg aggagctgcc   1200

ctggacttga gtcccttgca tcggagtccc catccctccc gccaagccat attctgttgg   1260

atgagcttca gtgcctacca gacagccttt atctgccttg ggctcctggt gcagcagatc   1320

atcttcttcc tgggaaccac ggccctggcc ttcctggtgc tcatgcctgt gctccatggc   1380

aggaacctcc tgctcttccg ttccctggag tcctcgtggc ccttctggct gactttggcc   1440

ctggctgtga tcctgcagaa catggcagcc cattgggtct tcctggagac tcatgatgga   1500

cacccacagc tgaccaaccg gcgagtgctc tatgcagcca cctttcttct cttccccctc   1560

aatgtgctgg tgggtgccat ggtggccacc tggcgagtgc tcctctctgc cctctacaac   1620

gccatccacc ttggccagat ggacctcagc ctgctgccac cgagagccgc cactctcgac   1680

cccggctact acacgtaccg aaacttcttg aagattgaag tcagccagtc gcatccagcc   1740

atgacagcct tctgctccct gctcctgcaa gcgcagagcc tcctacccag gaccatggca   1800

gcccccccagg acagcctcag accaggggag gaagacgaag gatgcagct gctacagaca   1860

aaggactcca tggccaaggg agctaggccc ggggccagcc gcggcagggc tcgctggggt   1920

ctggcctaca cgctgctgca caacccaacc ctgcaggtct tccgcaagac ggccctgttg   1980
```

ggtgccaatg gtgcccagcc c   2001

<210> 47

<211> 1392

<212> DNA

<213> Homo sapiens

<400> 47

atgattgtct gcctcctttt catgatgatt ttattggcaa aggaagttca actggtagac   60

caaacagatt cacctttact tagtctcctt ggacagacaa gctcactttc atggcatctt   120

gtggatattg tgtcgtacca gagtgtgcta agttatttca gcagccatta cccgccgtcc   180

atcatcctgg caaaagaatc ttatgctgaa ttaatcatga agctcctaaa agtgtctgcg   240

ggcctttcta ttcctactga cagccagaag catcttgatg cagttccaaa atgccaagct   300

tttactcatc agatggttca attcctcagc accctggaac aaaatggaaa aatcacctta   360

gcagtcctag aacaggaaat gtctaagctc ttagacgata tcattgtctt taacccgccc   420

gacatggaca gccagacccg ccacatggcc ctcagcagcc tctttatgga agtcctgatg   480

atgatgaaca acgcgactat tccaacagca gagttccttc ggggcagtat ccggacctgg   540

attggccaaa aaatgcatgg gctggtggtg ctgccccttt taacagcagc ctgccagagc   600

ctggcgtccg tccgccacat ggctgagact acagaagcct gcatcactgc ctacttcaaa   660

gaaagccctc tcaatcagaa ttcaggatgg ggacccattc tggtatccct tcaggttccc   720

gagctcacca tggaagagtt cctgcaggag tgcctcacct tgggcagtta cttgactctt   780

tacgtctact tgcttcagtg tttaaacagc gaacagactt taaggaatga aatgaaagtg   840

ctgctcatct taagcaagtg gctggaacag gtgtacccaa gctccgtgga ggaagaggca   900

aagctgtttt tgtggtggca ccaagtcctt cagctctccc tcattcagac agagcagaat   960

gactccgtcc tgacagaatc tgtcattcga attctgctct tggttcagag caggcagaac   1020

ctcgtggctg aggagagact cagctctggg atcctggggg caattgggtt tggccggaag   1080

```
tcgcctttgt ctaacaggtt ccgagtggtt gcccgaagca tggctgcctt cctttcagtt    1140

caggttccta tggaagatca gatccgtttg aggcctggct ctgaattaca tctgaccccc    1200

aaagctcagc aggctctgaa tgctcttgaa tccatggcat caagtaagca gtatgttgaa    1260

taccaggatc aaatattgca agccacccaa tttataaggc atcctggcca ttgccttcaa    1320

gatgggaaaa gcttcttggc tcttctcgtt aactgtctgt atccagaagt gcattatttg    1380

gaccacatac ga                                                        1392
```

<210> 48

<211> 1410

<212> DNA

<213> Homo sapiens

<400> 48

```
atgtctagac tgggagccct gggtggtgcc cgtgccgggc tgggactgtt gctgggtacc      60

gccgccggcc ttggattcct gtgcctcctt tacagccagc gatggaaacg gacccagcgt     120

catggccgca gccagagcct gcccaactcc ctggactata cgcagacttc agatcccgga     180

cgccacgtga tgctcctgcg ggctgtccca ggtggggctg gagatgcctc agtgctgccc     240

agccttccac gggaaggaca ggagaaggtg ctggaccgcc tggactttgt gctgaccagc     300

cttgtggcgc tgcggcggga ggtggaggag ctgagaagca gcctgcgagg gcttgcgggg     360

gagattgttg gggaggtccg atgccacatg gaagagaacc agagagtggc tcggcggcga     420

aggtttccgt ttgtccggga gaggagtgac tccactggct ccagctctgt ctacttcacg     480

gcctcctcgg gagccacgtt cacagatgct gagagtgaag ggggttacac aacagccaat     540

gcggagtctg acaatgagcg ggactctgac aaagaaagtg aggacggggga agatgaagtg     600

agctgtgaga ctgtgaagat ggggagaaag gattctcttg acttggagga agaggcagct     660

tcaggtgcct ccagtgccct ggaggctgga ggttcctcag gcttggagga tgtgctgccc     720

ctcctgcagc aggccgacga gctgcacagg ggtgatgagc aaggcaagcg ggagggcttc     780
```

```
cagctgctgc tcaacaacaa gctggtgtat ggaagccggc aggactttct ctggcgcctg    840

gccccgagcct acagtgacat gtgtgagctc actgaggagg tgagcgagaa gaagtcatat    900

gccctagatg gaaaagaaga agcagaggct gctctggaga aggggggatga gagtgctgac    960

tgtcacctgt ggtatgcggt gctttgtggt cagctggctg agcatgagag catccagagg   1020

cgcatccaga gtggctttag cttcaaggag catgtggaca aagccattgc tctccagcca   1080

gaaaacccca tggctcactt tcttcttggc aggtggtgct atcaggtctc tcacctgagc   1140

tggctagaaa aaaaaactgc tacagccttg cttgaaagcc ctctcagtgc cactgtggaa   1200

gatgccctcc agagcttcct aaaggctgaa gaactacagc caggattttc caaagcagga   1260

agggtatata tttccaagtg ctacagagaa ctaggaaaaa actctgaagc tagatggtgg   1320

atgaagttgg ccctggagct gccagatgtc acgaaggagg atttggctat ccagaaggac   1380

ctggaagaac tggaagtcat tttacgagac                                    1410
```

<210> 49

<211> 729

<212> DNA

<213> Homo sapiens

<400> 49

```
atggagcagg gcagcggccg cttggaggac ttccctgtca atgtgttctc cgtcactcct     60

tacacaccca gcaccgctga catccaggtg tccgatgatg acaaggcggg ggccaccttg    120

ctcttctcag gcatctttct gggactggtg gggatcacat tcactgtcat gggctggatc    180

aaataccaag gtgtctccca ctttgaatgg acccagctcc ttgggcccgt cctgctgtca    240

gttggggtga cattcatcct gattgctgtg tgcaagttca aaatgctctc ctgccagttg    300

tgcaaagaaa gtgaggaaag ggtcccggac tcggaacaga caccaggagg accatcattt    360

gttttcactg gcatcaacca acccatcacc ttccatgggg ccactgtggt gcagtacatc    420

cctcctcctt atggttctcc agagcctatg gggataaata ccagctacct gcagtctgtg    480
```

```
gtgagcccct gcggcctcat aacctctgga ggggcagcag ccgccatgtc aagtcctcct      540

caatactaca ccatctaccc tcaagataac tctgcatttg tggttgatga gggctgcctt      600

tctttcacgg acggtggaaa tcacaggccc aatcctgatg ttgaccagct agaagagaca      660

cagctggaag aggaggcctg tgcctgcttc tctcctcccc cttatgaaga aatatactct      720

ctccctcgc                                                             729
```

<210> 50

<211> 810

<212> DNA

<213> Homo sapiens

<400> 50

```
atggcgggcg ccgaggactg gccgggccag cagctggagc tggacgagga cgaggcgtct       60

tgttgccgct ggggcgcgca gcacgccggg gcccgcgagc tggctgcgct ctactcgcca      120

ggcaagcgcc tccaggagtg gtgctctgtg atcctgtgct tcagcctcat cgcccacaac      180

ctggtccatc tcctgctgct ggcccgctgg gaggacacac ccctcgtcat actcggtgtt      240

gttgcagggg ctctcattgc tgacttcttg tctggcctgg tacactgggg tgctgacaca      300

tggggctctg tggagctgcc cattgtgggg aaggctttca tccgacccTt ccgggagcac      360

cacattgacc caacagctat cacacggcac gacttcatcg agaccaacgg ggacaactgc      420

ctggtgacac tgctgccgct gctaaacatg gcctacaagt ccgcacccca gccctgaa       480

gccctggagc agctataccc ctgggagtgc ttcgtcttct gcctgatcat cttcggcacc      540

ttcaccaacc agatccacaa gtggtcgcac acgtactttg gctgccacg ctgggtcacc      600

ctcctgcagg actggcatgt catcctgcca cgtaaacacc atcgcatcca ccacgtctca      660

ccccacgaga cctacttctg catcaccaca ggctggctca actaccctct ggagaagata      720

ggcttctggc gacgcctgga ggacctcatc cagggcctga cgggcgagaa gcctcgggca      780

gatgacatga aatgggccca gaagatcaaa                                     810
```

<210> 51

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (98)... (1231)

<400> 51

```
caaggggaac gtggctttcc ctgcagagcc ggtgtctccg cctgcgtccc tgctgcagca      60

accggagctg gagtcggatc ccgaacgcac cctcgcc atg gac tcg gcc ctc agc     115
                                          Met Asp Ser Ala Leu Ser
                                            1               5

gat ccg cat aac ggc agt gcc gag gca ggc ggc ccc acc aac agc act      163
Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly Pro Thr Asn Ser Thr
          10              15              20

acg cgg ccg cct tcc acg ccc gag ggc atc gcg ctg gcc tac ggc agc      211
Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala Leu Ala Tyr Gly Ser
      25              30              35

ctc ctc ctc atg gcg ctg ctg ccc atc ttc ttc ggc gcc ctg cgc tcc      259
Leu Leu Leu Met Ala Leu Leu Pro Ile Phe Phe Gly Ala Leu Arg Ser
      40              45              50

gta cgc tgc gcc cgc ggc aag aat gct tca gac atg cct gaa aca atc      307
Val Arg Cys Ala Arg Gly Lys Asn Ala Ser Asp Met Pro Glu Thr Ile
55              60              65              70
```

acc agc cgg gat gcc gcc cgc ttc ccc atc atc gcc agc tgc aca ctc   355
Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile Ala Ser Cys Thr Leu
            75   80   85

ttg ggg ctc tac ctc ttt ttc aaa ata ttc tcc cag gag tac atc aac   403
Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser Gln Glu Tyr Ile Asn
            90   95   100

ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga atc ctg gcc ctg tcc   451
Leu Leu Leu Ser Met Tyr Phe Phe Val Leu Gly Ile Leu Ala Leu Ser
           105   110   115

cac acc atc agc ccc ttc atg aat aag ttt ttt cca gcc agc ttt cca   499
His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe Pro Ala Ser Phe Pro
       120   125   130

aat cga cag tac cag ctg ctc ttc aca cag ggt tct ggg gaa aac aag   547
Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly Ser Gly Glu Asn Lys
135   140   145   150

gaa gag atc atc aat tat gaa ttt gac acc aag gac ctg gtg tgc ctg   595
Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys Asp Leu Val Cys Leu
                155   160   165

ggc ctg agc agc atc gtt ggc gtc tgg tac ctg ctg agg aag cac tgg   643
Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu Leu Arg Lys His Trp
            170   175   180

att gcc aac aac ctt ttt ggc ctg gcc ttc tcc ctt aat gga gta gag   691
Ile Ala Asn Asn Leu Phe Gly Leu Ala Phe Ser Leu Asn Gly Val Glu
            185   190   195

ctc ctg cac ctc aac aat gtc agc act ggc tgc atc ctg ctg ggc gga   739

Leu Leu His Leu Asn Asn Val Ser Thr Gly Cys Ile Leu Leu Gly Gly

　　　200　　　　　　　　　205　　　　　　　210

ctc ttc atc tac gat gtc ttc tgg gta ttt ggc acc aat gtg atg gtg　　　787

Leu Phe Ile Tyr Asp Val Phe Trp Val Phe Gly Thr Asn Val Met Val

215　　　　　　　220　　　　　　　225　　　　　　　230

aca gtg gcc aag tcc ttc gag gca cca ata aaa ttg gtg ttt ccc cag　　　835

Thr Val Ala Lys Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln

　　　　　　235　　　　　　　240　　　　　　　245

gat ctg ctg gag aaa ggc ctc gaa gca aac aac ttt gcc atg ctg gga　　　883

Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly

　　　　　　250　　　　　　　255　　　　　　　260

ctt gga gat gtc gtc att cca ggg atc ttc att gcc ttg ctg ctg cgc　　　931

Leu Gly Asp Val Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg

　　　　　　265　　　　　　　270　　　　　　　275

ttt gac atc agc ttg aag aag aat acc cac acc tac ttc tac acc agc　　　979

Phe Asp Ile Ser Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser

　　　280　　　　　　　285　　　　　　　290

ttt gca gcc tac atc ttc ggc ctg ggc ctt acc atc ttc atc atg cac　　　1027

Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His

295　　　　　　　300　　　　　　　305　　　　　　　310

atc ttc aag cat gct cag cct gcc ctc cta tac ctg gtc ccc gcc tgc　　　1075

Ile Phe Lys His Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys

　　　　　　315　　　　　　　320　　　　　　　325

atc ggt ttt cct gtc ctg gtg gcg ctg gcc aag gga gaa gtg aca gag　　　1123

Ile Gly Phe Pro Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu

```
          330                335                340
atg ttc agt tat gag gag tca aat cct aag gat cca gcg gca gtg aca      1171
Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr

              345                350                355
gaa tcc aaa gag gga aca gag gca tca gca tcg aag ggg ctg gag aag      1219
Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys

              360                365                370
aaa gag aaa tg atgcagctgg tgcccgagcc tctcagggcc agaccagaca          1270
Lys Glu Lys

375
gatggggggct gggcccacac aggcgtgcac cggtagaggg cacaggaggc caagggcagc   1330

tccaggacag ggcaggggggc agcaggatac ctccagccag gcctctgtgg cctctgtttc   1390

cttctccctt tcttggccct cctctgctcc tccccacacc ctgcaggcaa aagaaacccc   1450

cagcttcccc cctccccggg agccaggtgg gaaaagtggg tgtgattttt agattttgta   1510

ttgtggactg attttgcctc acattaaaaa ctcatcccat g                       1551
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<210> 52

<211> 1713

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)... (334)

<400> 52

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tctcagcgcg ctgcccggct ggggacccgc gcacctgcag cgcccgctgc tcggccctgc   60
```

```
atcctgcctg ggcatcctgc gcccggcc atg acg gcg cac tca ttc gcc ctc        112
                                 Met Thr Ala His Ser Phe Ala Leu
                                  1               5

ccg gtc atc atc ttc acc acg ttc tgg ggc ctc gtc ggc atc gcc ggg       160
Pro Val Ile Ile Phe Thr Thr Phe Trp Gly Leu Val Gly Ile Ala Gly
     10              15              20

ccc tgg ttc gtg ccg aag gga ccc aac cgc gga gtg atc atc acc atg       208
Pro Trp Phe Val Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met
 25              30              35              40

ctg gtc gcc acc gcc gtc tgc tgt tac ctc ttc tgg ctc atc gcc atc       256
Leu Val Ala Thr Ala Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile
             45              50              55

ctg gcg cag ctg aac ccc ctg ttc ggg ccc cag ctg aag aat gag acc       304
Leu Ala Gln Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr
             60              65              70

atc tgg tac gtg cgc ttc ctg tgg gag tgacccgcc gcccccgacc             350
Ile Trp Tyr Val Arg Phe Leu Trp Glu
             75              80

caggtgccca gctctcggaa tgactgtggc tccactgtcc ctgacaaccc cttcgtccgg    410
accctccccc acacaactat gtctggtcac cagctccctc ctgctggcac ccagagaccc    470
ggacccgcag ggcctgcctg gttcctggaa gtcttcccag tcttcccagc cagcccgggc    530
cctggggagc cctgggcaca gcagcggccg aggggatgtc ctgctccaat acccgcactg    590
ctctggagtt tgccctcttt cccaaggaga tgctgctggg gagctggtat gggtggggtc    650
tttcccttta cagacggggc agatgccagg actcagccca tcctgaggag gacacgtgtc    710
ctcatggaga gggtgctccg gcccaggcgg gggagtcagt gcccagtcag cagctctgcc    770
```

```
accatcctgc tgggaactgg gggggcctct attgggttat aggcaaggcc ttttctctgg    830

catggaattg ttaattttct gacacgtcta gatgtgaaat ttctgaaaat gttgaagcag    890

agaaacattc acacacaaaa agcaacatag tcatgtgggt ccagatggcc tcagtcctag    950

atgttggcac cctttgctgt gtctcctcag agtatcctgt tccgcctcct gccacctgga   1010

cctccctcag tggatgtctt ccctcccccg accccagcct gtcagtccga gcacagtgca   1070

ggtttggctc tgacttgggc ttttggctgc agtgggggtg gatttcagag cctctcatgg   1130

cagcatctaa gtgaccagag ctgggatgag agaggggaag gggcaatgtg agtggcgcta   1190

tgggacgggc cagccctgct cctgagccag ccccgccctc tgccccctgg ccctgggctc   1250

tgtgctaggg atggtgaaga atggggggcgt gccagcctgg caggagtggg aagcaacacg   1310

caggggtccc ggacctctcc agccttgccc tcacgcttac ccgagctccc agtgtggtta   1370

gcacagagct cacccacctt gcctggctcc cagctggggc ctgtcctcac tggtgctcca   1430

ggggaagaaa cgacagcctc acttctgtat ggactgctga tgtggcctgc catcctgttc   1490

agcgggcatt gtctttggag cagcaggaga ataggatgcc tctcactcac atgccagttc   1550

ctggctggcc agctgctcag ggctcaggct ggggcctccc attgacatcc tcccctaca   1610

ctccctctct gagcctccgt cgcccctcct gttgggtaag ggtgttgagt gtgacttgtg   1670

ctgaaaacct ggttcatata taataaataa tggtgatgaa aag                     1713
```

<210> 53

<211> 1758

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (190)...(1653)

<400> 53

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tttctagggt tggaccgtgc aggcacgggc ggtcagctgg gccgcagctc ctccggctct      60

gcagggtcac ggaggaagcc agctccccta gtccaggccg agcttgcact tgcgtcttgt     120

ctgctgctgc tgaaccaaga tttagctgtg cgccctcctt gcagtctcct ggaaccagca     180

ggaggaaac atg ggg gat act ggc ctg aga aag cgg aga gag gat gag        228
         Met Gly Asp Thr Gly Leu Arg Lys Arg Arg Glu Asp Glu
              1               5                   10

aag tcg atc cag agc caa gag cct aag acc acc agt ctc caa aag gag      276
Lys Ser Ile Gln Ser Gln Glu Pro Lys Thr Thr Ser Leu Gln Lys Glu
     15                  20                  25

ctg ggc ctc atc agt ggc atc tcc atc atc gtg ggc acc atc att ggc      324
Leu Gly Leu Ile Ser Gly Ile Ser Ile Ile Val Gly Thr Ile Ile Gly
 30                  35                  40                  45

tct ggg atc ttc gtt tcc ccc aag tct gtg ctc agc aac acg gaa gct      372
Ser Gly Ile Phe Val Ser Pro Lys Ser Val Leu Ser Asn Thr Glu Ala
                 50                  55                  60

gtg ggg ccc tgc ctc atc ata tgg gcg gct tgc ggg gtc ctc gcg acg      420
Val Gly Pro Cys Leu Ile Ile Trp Ala Ala Cys Gly Val Leu Ala Thr
                 65                  70                  75

ctg ggt gcc ctg tgc ttt gcg gag ctt ggc aca atg atc acc aag tca      468
Leu Gly Ala Leu Cys Phe Ala Glu Leu Gly Thr Met Ile Thr Lys Ser
                 80                  85                  90

ggg gga gag tat ccc tac ctg atg gag gcc tac ggg ccc atc ccc gcc      516
Gly Gly Glu Tyr Pro Tyr Leu Met Glu Ala Tyr Gly Pro Ile Pro Ala
     95                  100                 105

tac ctc ttc tcc tgg gcc agc ctg atc gtc att aag ccc acg tcc ttc      564
```

```
Tyr Leu Phe Ser Trp Ala Ser Leu Ile Val Ile Lys Pro Thr Ser Phe
110             115             120             125

gcc atc atc tgc ctc agc ttc tcc gag tat gtg tgt gcg ccc ttc tat      612
Ala Ile Ile Cys Leu Ser Phe Ser Glu Tyr Val Cys Ala Pro Phe Tyr
                130             135             140

gtg ggc tgc aag cct cct caa atc gtt gtg aaa tgc ctg gcc gcc gcc      660
Val Gly Cys Lys Pro Pro Gln Ile Val Val Lys Cys Leu Ala Ala Ala
                145             150             155

gcc atc ttg ttc atc tcg aca gtg aac tca ctg agc gtg cgg ctg gga      708
Ala Ile Leu Phe Ile Ser Thr Val Asn Ser Leu Ser Val Arg Leu Gly
                160             165             170

agc tac gtc cag aac atc ttc acc gcg gcc aag ctg gtg atc gtg gcc      756
Ser Tyr Val Gln Asn Ile Phe Thr Ala Ala Lys Leu Val Ile Val Ala
        175             180             185

atc atc atc atc agc ggg ctg gtg ctc ctg gcc caa gga aac aca aag      804
Ile Ile Ile Ile Ser Gly Leu Val Leu Leu Ala Gln Gly Asn Thr Lys
190             195             200             205

aat ttt gat aat tct ttc gag ggc gcc cag ctg tct gtg gga gcc atc      852
Asn Phe Asp Asn Ser Phe Glu Gly Ala Gln Leu Ser Val Gly Ala Ile
                210             215             220

agc ctg gcg ttt tac aat gga ctc tgg gcc tat gat gga tgg aat caa      900
Ser Leu Ala Phe Tyr Asn Gly Leu Trp Ala Tyr Asp Gly Trp Asn Gln
                225             230             235

ctc aat tac atc aca gaa gaa ctt aga aac cct tac aga aac ctg cct      948
Leu Asn Tyr Ile Thr Glu Glu Leu Arg Asn Pro Tyr Arg Asn Leu Pro
```

```
                240                   245                   250
ttg gcc att atc atc ggg atc ccc ctg gtg acg gcg tgc tac atc ctc     996
Leu Ala Ile Ile Ile Gly Ile Pro Leu Val Thr Ala Cys Tyr Ile Leu
        255                   260                   265
atg aac gtg tcc tac ttc acc gtg atg act gcc acc gaa ctc ctg cag    1044
Met Asn Val Ser Tyr Phe Thr Val Met Thr Ala Thr Glu Leu Leu Gln
270                   275                   280                   285
tcc cag gcg gtg gct gtg aca ttt ggt gac cgt gtt ctc tat cct gct    1092
Ser Gln Ala Val Ala Val Thr Phe Gly Asp Arg Val Leu Tyr Pro Ala
                      290                   295                   300
tct tgg atc gtt cca ctt ttt gtg gca ttt tca acc atc ggt gct gct    1140
Ser Trp Ile Val Pro Leu Phe Val Ala Phe Ser Thr Ile Gly Ala Ala
                      305                   310                   315
aac ggg acc tgc ttc aca gcg ggc aga ctc att tac gtg gcg ggc cgg    1188
Asn Gly Thr Cys Phe Thr Ala Gly Arg Leu Ile Tyr Val Ala Gly Arg
              320                   325                   330
gag ggt cac atg ctc aaa gtg ctt tct tac atc agc gtc agg cgc ctc    1236
Glu Gly His Met Leu Lys Val Leu Ser Tyr Ile Ser Val Arg Arg Leu
        335                   340                   345
act cca gcc ccc gcc atc atc ttt tat ggt atc ata gca acg att tat    1284
Thr Pro Ala Pro Ala Ile Ile Phe Tyr Gly Ile Ile Ala Thr Ile Tyr
350                   355                   360                   365
atc atc cct ggt gac ata aac tcg tta gtc aat tat ttc agc ttt gcc    1332
Ile Ile Pro Gly Asp Ile Asn Ser Leu Val Asn Tyr Phe Ser Phe Ala
              370                   375                   380
```

```
gca tgg ctg ttt tat ggc ctg acg att cta gga ctc atc gtg atg aga        1380
Ala Trp Leu Phe Tyr Gly Leu Thr Ile Leu Gly Leu Ile Val Met Arg
         385                 390                 395

ttt aca agg aaa gag ctg gaa agg cct atc aag gtg ccc gta gtc att        1428
Phe Thr Arg Lys Glu Leu Glu Arg Pro Ile Lys Val Pro Val Val Ile
         400                 405                 410

ccc gtc ttg atg aca ctc atc tct gtg ttt ttg gtt ctg gct cca atc        1476
Pro Val Leu Met Thr Leu Ile Ser Val Phe Leu Val Leu Ala Pro Ile
         415                 420                 425

atc agc aag ccc acc tgg gag tac ctc tac tgt gtg ctg ttt ata tta       .1524
Ile Ser Lys Pro Thr Trp Glu Tyr Leu Tyr Cys Val Leu Phe Ile Leu
430                 435                 440                 445

agc ggc ctt tta ttt tac ttc ctg ttt gtc cac tac aag ttt gga tgg        1572
Ser Gly Leu Leu Phe Tyr Phe Leu Phe Val His Tyr Lys Phe Gly Trp
         450                 455                 460

gct cag aaa atc tca aag ccg att acc atg cac ctt cag atg cta atg        1620
Ala Gln Lys Ile Ser Lys Pro Ile Thr Met His Leu Gln Met Leu Met
         465                 470                 475

gaa gtg gtc cca ccg gag gaa gac cct gag taacaagctc cgtctcttgt          1670
Glu Val Val Pro Pro Glu Glu Asp Pro Glu
         480                 485

agccaagtca gctgaattta ttttcttaag caatatttgt ggttatttct tccttttttt      1730
cttacgaata aaatatactc agatgttt                                         1758
```

<210> 54

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (154)...(1281)

<400> 54

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ctctgtttac cgagagagcc cgtccaagtt gggctccatc gctgccctcg ctccccttcg      60

gggcctccgc ccgcctggga agcagagaga aagccgggcc cagcccttcc tcacccttcc     120

cctccccgca ccgcccggag aggtcggacg gcg atg acc ccc cag ccc gcc gga     174
                                       Met Thr Pro Gln Pro Ala Gly
                                         1               5

ccc ccg gat ggg ggc tgg ggc tgg gtg gtg gcg gcc gca gcc ttc gcg     222
Pro Pro Asp Gly Gly Trp Gly Trp Val Val Ala Ala Ala Ala Phe Ala
           10               15               20

ata aac ggg ctg tcc tac ggg ctg ctg cgc tcg ctg ggc ctt gcc ttc     270
Ile Asn Gly Leu Ser Tyr Gly Leu Leu Arg Ser Leu Gly Leu Ala Phe
       25               30               35

cct gac ctt gcc gag cac ttt gac cga agc gcc cag gac act gcg tgg     318
Pro Asp Leu Ala Glu His Phe Asp Arg Ser Ala Gln Asp Thr Ala Trp
   40               45               50               55

atc agc gcc ctg gcc ctg gcc gtg cag cag gca gcc agc ccc gtg ggc     366
Ile Ser Ala Leu Ala Leu Ala Val Gln Gln Ala Ala Ser Pro Val Gly
           60               65               70

agc gcc ctg agc acg cgc tgg ggg gcc cgc ccc gtg gtg atg gtt ggg     414
Ser Ala Leu Ser Thr Arg Trp Gly Ala Arg Pro Val Val Met Val Gly
```

Ser Ala Leu Ser Thr Arg Trp Gly Ala Arg Pro Val Val Met Val Gly

         75   80   85

ggc gtc ctc gcc tcg ctg ggc ttc gtc ttc tcg gct ttc gcc agc ggt   462

Gly Val Leu Ala Ser Leu Gly Phe Val Phe Ser Ala Phe Ala Ser Gly

         90   95   100

ctg ctg cat ctc tac ctc ggc ctg ggc ctc ctc gct ggc ttt ggt tgg   510

Leu Leu His Leu Tyr Leu Gly Leu Gly Leu Leu Ala Gly Phe Gly Trp

     105   110   115

gcc ctg gtg ttc gcc ccc gcc cta ggc acc ctc tcg cgt tac ttc tcc   558

Ala Leu Val Phe Ala Pro Ala Leu Gly Thr Leu Ser Arg Tyr Phe Ser

120   125   130   135

cgc cgt cga gtc ttg gcg gtg ggg ctg gcg ctc acc ggc aac ggg gcc   606

Arg Arg Arg Val Leu Ala Val Gly Leu Ala Leu Thr Gly Asn Gly Ala

     140   145   150

tcc tcg ctg ctc ctg gcg ccc gcc ttg cag ctt ctc ctc gat act ttc   654

Ser Ser Leu Leu Leu Ala Pro Ala Leu Gln Leu Leu Leu Asp Thr Phe

     155   160   165

ggc tgg cgg ggc gct ctg ctc ctc ctc ggc gcg atc acc ctc cac ctc   702

Gly Trp Arg Gly Ala Leu Leu Leu Leu Gly Ala Ile Thr Leu His Leu

     170   175   180

acc ccc tgt ggc gcc ctg ctg cta ccc ctg gtc ctt cct gga gac ccc   750

Thr Pro Cys Gly Ala Leu Leu Leu Pro Leu Val Leu Pro Gly Asp Pro

     185   190   195

cca gcc cca ccg cgt agt ccc cta gct gcc ctc ggc ctg agt ctg ttc   798

Pro Ala Pro Pro Arg Ser Pro Leu Ala Ala Leu Gly Leu Ser Leu Phe

```
                200                 205                 210                 215

aca cgc cgg gcc ttc tca atc ttt gct cta ggc aca gcc ctg gtt ggg     846
Thr Arg Arg Ala Phe Ser Ile Phe Ala Leu Gly Thr Ala Leu Val Gly
                    220                 225                 230

ggc ggg tac ttc gtt cct tac gtg cac ttg gct ccc cgc ttt aga ccg     894
Gly Gly Tyr Phe Val Pro Tyr Val His Leu Ala Pro Arg Phe Arg Pro
                    235                 240                 245

ggg cct ggg ggg ata cgg agc agc gct ggt ggt ggc cgt ggc tgc gat     942
Gly Pro Gly Gly Ile Arg Ser Ser Ala Gly Gly Gly Arg Gly Cys Asp
                250                 255                 260

ggg gga tgc ggg cgc ccg gct ggt ctg cgg gtg gct ggc aga cca agg     990
Gly Gly Cys Gly Arg Pro Ala Gly Leu Arg Val Ala Gly Arg Pro Arg
            265                 270                 275

ctg ggt gcc cct ccc gcg gct gct ggc cgt att cgg ggc tct gac tgg    1038
Leu Gly Ala Pro Pro Ala Ala Ala Gly Arg Ile Arg Gly Ser Asp Trp
280                 285                 290                 295

gct ggg gct gtg ggt ggt ggg gct ggt gcc cgt ggt ggg cgg cga aga    1086
Ala Gly Ala Val Gly Gly Gly Ala Gly Ala Arg Gly Gly Arg Arg Arg
                    300                 305                 310

gag ctg ggg ggg tcc cct gct ggc cgc ggc tgt ggc cta tgg gct gag    1134
Glu Leu Gly Gly Ser Pro Ala Gly Arg Gly Cys Gly Leu Trp Ala Glu
                    315                 320                 325

cgc ggg gag tta cgc ccc gct ggt ttt cgg tgt act ccc cgg gct ggt    1182
Arg Gly Glu Leu Arg Pro Ala Gly Phe Arg Cys Thr Pro Arg Ala Gly
                330                 335                 340
```

```
ggg cgt cgg agg tgt ggt gca ggc cac agg gct ggt gat gat gct gat       1230
Gly Arg Arg Arg Cys Gly Ala Gly His Arg Ala Gly Asp Asp Ala Asp
        345                 350                 355

gag cct cgg ggg gct cct ggg ccc tcc cct gtc agg ctt cct aag gga       1278
Glu Pro Arg Gly Ala Pro Gly Pro Ser Pro Val Arg Leu Pro Lys Gly
360                 365                 370                 375

tg agacaggaga cttcaccgcc tctttcctcc tgtctggttc tttgatcctc            1330

tccggcagct tcatctacat agggttgccc agggcgctgc cctcctgtgg tccagcctcc    1390

cctccagcca cgcctccccc agagacgggg gagctgcttc ccgctcccca ggcagtcttg    1450

ctgtccccag gaggccctgg ctccactctg dacaccactt gttgattatt ttcttgtttg    1510

agcccctccc ccaataaaga attttttatcg ggttttcctg                          1550
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<210> 55

<211> 1485

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (101)...(1153)

<400> 55

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ctctcctcga ccctggacgt ctaccttccg gaggcccaca tcttgcccac tccgcgcgcg     60

gggctagcgc gggtttcagc gacgggagcc ctcaagggac atg gca act aca gcg      115
                                                Met Ala Thr Thr Ala
                                                 1               5

gcg ccg gcg ggc ggc gcc cga aat gga gct ggc ccg gaa tgg gga ggg      163
```

Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly Pro Glu Trp Gly Gly
                    10   15   20

ttc gaa gaa aac atc cag ggc gga ggc tca gct gtg att gac atg gag   211
Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala Val Ile Asp Met Glu
                    25   30   35

aac atg gat gat acc tca ggc tct agc ttc gag gat atg ggt gag ctg   259
Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu Asp Met Gly Glu Leu
                    40   45   50

cat cag cgc ctg cgc gag gaa gaa gta gac gct gat gca gct gat gca   307
His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala Asp Ala Ala Asp Ala
        55   60   65

gct gct gct gaa gag gag gat gga gag ttc ctg ggc atg aag ggc ttt   355
Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu Gly Met Lys Gly Phe
    70   75   80   85

aag gga cag ctg agc cgg cag gtg gca gat cag atg tgg cag gct ggg   403
Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln Met Trp Gln Ala Gly
                    90   95   100

aaa aga caa gcc tcc agg gcc ttc agc ttg tac gcc aac atc gac atc   451
Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr Ala Asn Ile Asp Ile
                    105   110   115

ctc aga ccc tac ttt gat gtg gag cct gct cag gtg cga agc agg ctc   499
Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln Val Arg Ser Arg Leu
                    120   125   130

ctg gag tcc atg atc cct atc aag atg gtc aac ttc ccc cag aaa att   547
Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn Phe Pro Gln Lys Ile

                        135   140   145

gca ggt gaa ctc tat gga cct ctc atg ctg gtc ttc act ctg gtt gct   595
Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala
150   155   160   165

atc cta ctc cat ggg atg aag acg tct gac act att atc cgg gag ggc   643
Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly
                        170   175   180

acc ctg atg ggc aca gcc att ggc acc tgc ttc ggc tac tgg ctg gga   691
Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly
                        185   190   195

gtc tca tcc ttc att tac ttc ctt gcc tac ctg tgc aac gcc cag atc   739
Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile
            200   205   210

acc atg ctg cag atg ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat   787
Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His
            215   220   225

tgc att gtc ctg ttc atc acc tat aat atc cac ctc cac gcc ctc ttc   835
Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His Leu His Ala Leu Phe
230   235   240   245

tac ctc ttc tgg ctg ttg gtg ggt gga ctg tcc aca ctg cgc atg gta   883
Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val
            250   255   260

gca gtg ttg gtg tct cgg acc gtg ggc ccc aca cag cgg ctg ctc ctc   931
Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr Gln Arg Leu Leu Leu
            265   270   275

```
tgt ggc acc ctg gct gcc cta cac atg ctc ttc ctg ctc tat ctg cat          979
Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe Leu Leu Tyr Leu His
        280             285             290

ttt gcc tac cac aaa gtg gta gag ggg atc ctg gac aca ctg gag ggc          1027
Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu Asp Thr Leu Glu Gly
        295             300             305

ccc aac atc ccg ccc atc cag agg gtc ccc aga gac atc cct gcc atg          1075
Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met
310             315             320             325

ctc cct gct gct cgg ctt ccc acc acc gtc ctc aac gcc aca gcc aaa          1123
Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys
            330             335             340

gct gtt gcg gtg acc ctg cag tca cac tgaccccacc tgaaattctt              1170
Ala Val Ala Val Thr Leu Gln Ser His
        345             350

ggccagtcct ctttcccgca gctgcagaga ggaggaagac tattaaagga cagtcctgat       1230
gacatgtttc gtagatgggg tttgcagctg ccactgagct gtagctgcgt aagtacctcc       1290
ttgatgcctg tcggcacttc tgaaaggcac aaggccaaga actcctggcc aggactgcaa       1350
ggctctgcag ccaatgcaga aaatgggtca gctcctttga gaacccctcc ccacctaccc       1410
cttccttcct ctttatctct cccacattgt cttgctaaat atagacttgg taattaaaat       1470
gttgattgaa gtctg                                                         1485
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<210> 56

<211> 2694

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (80)... (2083)

<400> 56

gtagactctg cggatcccga gaccagcgcc actcatcctg cagcactggg gacagacaga   60

gcaggagaag ggccagaga atg tcg tcc cag cca gca ggg aac cag acc tcc   112
                     Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser
                      1   5   10

ccc ggg gcc aca gag gac tac tcc tat ggc agc tgg tac atc gat gag   160
Pro Gly Ala Thr Glu Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu
            15   20   25

ccc cag ggg ggc gag gag ctc cag cca gag ggg gaa gtg ccc tcc tgc   208
Pro Gln Gly Gly Glu Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys
            30   35   40

cac acc agc ata cca ccc ggc ctg tac cac gcc tgc ctg gcc tcg ctg   256
His Thr Ser Ile Pro Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu
            45   50   55

tca atc ctt gtg ctg ctg ctc ctg gcc atg ctg gtg agg cgc cgc cag   304
Ser Ile Leu Val Leu Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln
60   65   70   75

ctc tgg cct gac tgt gtg cgt ggc agg ccc ggc ctg ccc agc cct gtg   352
Leu Trp Pro Asp Cys Val Arg Gly Arg Pro Gly Leu Pro Ser Pro Val
                80   85   90

gat ttc ttg gct ggg gac agg ccc cgg gca gtg cct gct gct gtt ttc   400

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Asp Phe Leu Ala Gly Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe
         95                  100                  105

atg gtc ctc ttg agc tcc ctg tgt ttg ctg ctc ccc gac gag gac gca    448
Met Val Leu Leu Ser Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala
         110                  115                  120

ttg ccc ttc ctg act ctc gcc tca gca ccc agc caa gat ggg aaa act    496
Leu Pro Phe Leu Thr Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr
     125                  130                  135

gag gct cca aga ggg gcc tgg aag ata ctg gga ctg ttc tat tat gct    544
Glu Ala Pro Arg Gly Ala Trp Lys Ile Leu Gly Leu Phe Tyr Tyr Ala
140                  145                  150                  155

gcc ctc tac tac cct ctg gct gcc tgt gcc acg gct ggc cac aca gct    592
Ala Leu Tyr Tyr Pro Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala
                 160                  165                  170

gca cac ctg ctc ggc agc acg ctg tcc tgg gcc cac ctt ggg gtc cag    640
Ala His Leu Leu Gly Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln
             175                  180                  185

gtc tgg cag agg gca gag tgt ccc cag gtg ccc aag atc tac aag tac    688
Val Trp Gln Arg Ala Glu Cys Pro Gln Val Pro Lys Ile Tyr Lys Tyr
         190                  195                  200

tac tcc ctg ctg gcc tcc ctg cct ctc ctg ctg ggc ctc gga ttc ctg    736
Tyr Ser Leu Leu Ala Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu
     205                  210                  215

agc ctt tgg tac cct gtg cag ctg gtg aga agc ttc agc cgt agg aca    784
Ser Leu Trp Tyr Pro Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr
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        220                 225                 230                 235

gga gca ggc tcc aag ggg ctg cag agc agc tac tct gag gaa tat ctg          832
Gly Ala Gly Ser Lys Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu

                240                 245                 250

agg aac ctc ctt tgc agg aag aag ctg gga agc agc tac cac acc tcc          880
Arg Asn Leu Leu Cys Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser

            255                 260                 265

aag cat ggc ttc ctg tcc tgg gcc cgc gtc tgc ttg aga cac tgc atc          928
Lys His Gly Phe Leu Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile

            270                 275                 280

tac act cca cag cca gga ttc cat ctc ccg ctg aag ctg gtg ctt tca          976
Tyr Thr Pro Gln Pro Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser

        285                 290                 295

gct aca ctg aca ggg acg gcc att tac cag gtg gcc ctg ctg ctg ctg         1024
Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu Leu Leu Leu
300                 305                 310                 315

gtg ggc gtg gta ccc act atc cag aag gtg agg gca ggg gtc acc acg         1072
Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly Val Thr Thr

                320                 325                 330

gat gtc tcc tac ctg ctg gcc ggc ttt gga atc gtg ctc tcc gag gac         1120
Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp

            335                 340                 345

aag cag gag gtg gtg gag ctg gtg aag cac cat ctg tgg gct ctg gaa         1168
Lys Gln Glu Val Val Glu Leu Val Lys His His Leu Trp Ala Leu Glu

        350                 355                 360
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gtg tgc tac atc tca gcc ttg gtc ttg tcc tgc tta ctc acc ttc ctg   1216
Val Cys Tyr Ile Ser Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu
    365   370   375

gtc ctg atg cgc tca ctg gtg aca cac agg acc aac ctt cga gct ctg   1264
Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu Arg Ala Leu
380   385   390   395

cac cga gga gct gcc ctg gac ttg agt ccc ttg cat cgg agt ccc cat   1312
His Arg Gly Ala Ala Leu Asp Leu Ser Pro Leu His Arg Ser Pro His
          400   405   410

ccc tcc cgc caa gcc ata ttc tgt tgg atg agc ttc agt gcc tac cag   1360
Pro Ser Arg Gln Ala Ile Phe Cys Trp Met Ser Phe Ser Ala Tyr Gln
          415   420   425

aca gcc ttt atc tgc ctt ggg ctc ctg gtg cag cag atc atc ttc ttc   1408
Thr Ala Phe Ile Cys Leu Gly Leu Leu Val Gln Gln Ile Ile Phe Phe
          430   435   440

ctg gga acc acg gcc ctg gcc ttc ctg gtg ctc atg cct gtg ctc cat   1456
Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro Val Leu His
    445   450   455

ggc agg aac ctc ctg ctc ttc cgt tcc ctg gag tcc tcg tgg ccc ttc   1504
Gly Arg Asn Leu Leu Leu Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe
460   465   470   475

tgg ctg act ttg gcc ctg gct gtg atc ctg cag aac atg gca gcc cat   1552
Trp Leu Thr Leu Ala Leu Ala Val Ile Leu Gln Asn Met Ala Ala His
          480   485   490

tgg gtc ttc ctg gag act cat gat gga cac cca cag ctg acc aac cgg   1600

Trp Val Phe Leu Glu Thr His Asp Gly His Pro Gln Leu Thr Asn Arg

           495   500   505

cga gtg ctc tat gca gcc acc ttt ctt ctc ttc ccc ctc aat gtg ctg   1648

Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu

           510   515   520

gtg ggt gcc atg gtg gcc acc tgg cga gtg ctc ctc tct gcc ctc tac   1696

Val Gly Ala Met Val Ala Thr Trp Arg Val Leu Leu Ser Ala Leu Tyr

         525   530   535

aac gcc atc cac ctt ggc cag atg gac ctc agc ctg ctg cca ccg aga   1744

Asn Ala Ile His Leu Gly Gln Met Asp Leu Ser Leu Leu Pro Pro Arg

540   545   550   555

gcc gcc act ctc gac ccc ggc tac tac acg tac cga aac ttc ttg aag   1792

Ala Ala Thr Leu Asp Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys

           560   565   570

att gaa gtc agc cag tcg cat cca gcc atg aca gcc ttc tgc tcc ctg   1840

Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe Cys Ser Leu

           575   580   585

ctc ctg caa gcg cag agc ctc cta ccc agg acc atg gca gcc ccc cag   1888

Leu Leu Gln Ala Gln Ser Leu Leu Pro Arg Thr Met Ala Ala Pro Gln

         590   595   600

gac agc ctc aga cca ggg gag gaa gac gaa ggg atg cag ctg cta cag   1936

Asp Ser Leu Arg Pro Gly Glu Glu Asp Glu Gly Met Gln Leu Leu Gln

         605   610   615

aca aag gac tcc atg gcc aag gga gct agg ccc ggg gcc agc cgc ggc   1984

Thr Lys Asp Ser Met Ala Lys Gly Ala Arg Pro Gly Ala Ser Arg Gly

```
          620                 625                 630                 635
agg gct cgc tgg ggt ctg gcc tac acg ctg ctg cac aac cca acc ctg        2032
Arg Ala Arg Trp Gly Leu Ala Tyr Thr Leu Leu His Asn Pro Thr Leu
                    640                 645                 650
cag gtc ttc cgc aag acg gcc ctg ttg ggt gcc aat ggt gcc cag ccc        2080
Gln Val Phe Arg Lys Thr Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro
               655                 660                 665
 tgagggcagg gaaggtcaac ccacctgccc atctgtgctg aggcatgttc               2130
ctgcctacca tcctcctccc tccccggctc tcctcccagc atcacaccag ccatgcagcc      2190
agcaggtcct ccggatcacc gtggttgggt ggaggtctgt ctgcactggg agcctcagga      2250
gggctctgct ccacccactt ggctatggga gagccagcag gggttctgga gaaagaaact      2310
ggtgggttag ggccttggtc caggagccag ttgagccagg gcagccacat ccaggcgtct      2370
ccctaccctg gctctgccat cagccttgaa gggcctcgat gaagccttct ctggaaccac      2430
tccagcccag ctccacctca gccttggcct tcacgctgtg gaagcagcca aggcacttcc      2490
tcaccccctc agcgccacgg acctctctgg ggagtggccg gaaagctccc gggcctctgg      2550
cctgcagggc agcccaagtc atgactcaga ccaggtccca cactgagctg cccacactcg      2610
agagccagat atttttgtag tttttatgcc tttggctatt atgaaagagg ttagtgtgtt      2670
ccctgcaata aacttgttcc tgag                                            2694
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<211> 3297

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<213> Homo sapiens

<220>

<221> CDS

<222> (83)... (1477)

<400> 57

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tccccaccca gaaacccgca gc atg att gtc tgc ctc ctt ttc atg atg att   112
                          Met Ile Val Cys Leu Leu Phe Met Met Ile
                           1   5   10

tta ttg gca aag gaa gtt caa ctg gta gac caa aca gat tca cct tta   160
Leu Leu Ala Lys Glu Val Gln Leu Val Asp Gln Thr Asp Ser Pro Leu
                15   20   25

ctt agt ctc ctt gga cag aca agc tca ctt tca tgg cat ctt gtg gat   208
Leu Ser Leu Leu Gly Gln Thr Ser Ser Leu Ser Trp His Leu Val Asp
                30   35   40

att gtg tcg tac cag agt gtg cta agt tat ttc agc agc cat tac ccg   256
Ile Val Ser Tyr Gln Ser Val Leu Ser Tyr Phe Ser Ser His Tyr Pro
                45   50   55

ccg tcc atc atc ctg gca aaa gaa tct tat gct gaa tta atc atg aag   304
Pro Ser Ile Ile Leu Ala Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys
                60   65   70

ctc cta aaa gtg tct gcg ggc ctt tct att cct act gac agc cag aag   352
Leu Leu Lys Val Ser Ala Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys
75   80   85   90

cat ctt gat gca gtt cca aaa tgc caa gct ttt act cat cag atg gtt   400
His Leu Asp Ala Val Pro Lys Cys Gln Ala Phe Thr His Gln Met Val
                95   100   105

caa ttc ctc agc acc ctg gaa caa aat gga aaa atc acc tta gca gtc   448

Gln Phe Leu Ser Thr Leu Glu Gln Asn Gly Lys Ile Thr Leu Ala Val

                    110   115   120

cta gaa cag gaa atg tct aag ctc tta gac gat atc att gtc ttt aac   496

Leu Glu Gln Glu Met Ser Lys Leu Leu Asp Asp Ile Ile Val Phe Asn

                    125   130   135

ccg ccc gac atg gac agc cag acc cgc cac atg gcc ctc agc agc ctc   544

Pro Pro Asp Met Asp Ser Gln Thr Arg His Met Ala Leu Ser Ser Leu

           140   145   150

ttt atg gaa gtc ctg atg atg atg aac aac gcg act att cca aca gca   592

Phe Met Glu Val Leu Met Met Met Asn Asn Ala Thr Ile Pro Thr Ala

155   160   165   170

gag ttc ctt cgg ggc agt atc cgg acc tgg att ggc caa aaa atg cat   640

Glu Phe Leu Arg Gly Ser Ile Arg Thr Trp Ile Gly Gln Lys Met His

                    175   180   185

ggg ctg gtg gtg ctg ccc ctt tta aca gca gcc tgc cag agc ctg gcg   688

Gly Leu Val Val Leu Pro Leu Leu Thr Ala Ala Cys Gln Ser Leu Ala

               190   195   200

tcc gtc cgc cac atg gct gag act aca gaa gcc tgc atc act gcc tac   736

Ser Val Arg His Met Ala Glu Thr Thr Glu Ala Cys Ile Thr Ala Tyr

           205   210   215

ttc aaa gaa agc cct ctc aat cag aat tca gga tgg gga ccc att ctg   784

Phe Lys Glu Ser Pro Leu Asn Gln Asn Ser Gly Trp Gly Pro Ile Leu

           220   225   230

gta tcc ctt cag gtt ccc gag ctc acc atg gaa gag ttc ctg cag gag   832

Val Ser Leu Gln Val Pro Glu Leu Thr Met Glu Glu Phe Leu Gln Glu

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      235                240                245                250
tgc ctc acc ttg ggc agt tac ttg act ctt tac gtc tac ttg ctt cag       880
Cys Leu Thr Leu Gly Ser Tyr Leu Thr Leu Tyr Val Tyr Leu Leu Gln
                  255                260                265
tgt tta aac agc gaa cag act tta agg aat gaa atg aaa gtg ctg ctc       928
Cys Leu Asn Ser Glu Gln Thr Leu Arg Asn Glu Met Lys Val Leu Leu
                  270                275                280
atc tta agc aag tgg ctg gaa cag gtg tac cca agc tcc gtg gag gaa       976
Ile Leu Ser Lys Trp Leu Glu Gln Val Tyr Pro Ser Ser Val Glu Glu
                  285                290                295
gag gca aag ctg ttt ttg tgg tgg cac caa gtc ctt cag ctc tcc ctc      1024
Glu Ala Lys Leu Phe Leu Trp Trp His Gln Val Leu Gln Leu Ser Leu
                  300                305                310
att cag aca gag cag aat gac tcc gtc ctg aca gaa tct gtc att cga      1072
Ile Gln Thr Glu Gln Asn Asp Ser Val Leu Thr Glu Ser Val Ile Arg
315                320                325                330
att ctg ctc ttg gtt cag agc agg cag aac ctc gtg gct gag gag aga      1120
Ile Leu Leu Leu Val Gln Ser Arg Gln Asn Leu Val Ala Glu Glu Arg
                  335                340                345
ctc agc tct ggg atc ctg ggg gca att ggg ttt ggc cgg aag tcg cct      1168
Leu Ser Ser Gly Ile Leu Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro
                  350                355                360
ttg tct aac agg ttc cga gtg gtt gcc cga agc atg gct gcc ttc ctt      1216
Leu Ser Asn Arg Phe Arg Val Val Ala Arg Ser Met Ala Ala Phe Leu
            365                370                375
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tca gtt cag gtt cct atg gaa gat cag atc cgt ttg agg cct ggc tct    1264
Ser Val Gln Val Pro Met Glu Asp Gln Ile Arg Leu Arg Pro Gly Ser
    380             385             390

gaa tta cat ctg acc ccc aaa gct cag cag gct ctg aat gct ctt gaa    1312
Glu Leu His Leu Thr Pro Lys Ala Gln Gln Ala Leu Asn Ala Leu Glu
395             400             405             410

tcc atg gca tca agt aag cag tat gtt gaa tac cag gat caa ata ttg    1360
Ser Met Ala Ser Ser Lys Gln Tyr Val Glu Tyr Gln Asp Gln Ile Leu
            415             420             425

caa gcc acc caa ttt ata agg cat cct ggc cat tgc ctt caa gat ggg    1408
Gln Ala Thr Gln Phe Ile Arg His Pro Gly His Cys Leu Gln Asp Gly
            430             435             440

aaa agc ttc ttg gct ctt ctc gtt aac tgt ctg tat cca gaa gtg cat    1456
Lys Ser Phe Leu Ala Leu Leu Val Asn Cys Leu Tyr Pro Glu Val His
            445             450             455

tat ttg gac cac ata cga tagtta acactgaggc tcttgaaaaa cccattgctg    1510
Tyr Leu Asp His Ile Arg
        460

tttatgttta catttaactt tgctgttgca caagtaactt tgctcaattg cactgtagag    1570
ctcagtttgg ccaatgtgta gttgactgag atgcaagttg ggaggcgtta gatattagat    1630
aattttgggg tgtgtgtgtg tgtgtgtgtg tgttttctta gctcttaaga ccttctgggg    1690
actctttaag tttttatatt tatccacaag agaaacttac taagttccac ttgggtgcag    1750
agccactcac agttgccgaa tgtcccagtc atctcacaag acctccagat ggagttcttt    1810
gtatgtttcc acttctgtct ctgttttatg taaatgttcc agatctgaca accttggaag    1870
tcactcagta cccttacttt taaaccccat ttgtgttcct ccaaagtaaa gaagtcaatt    1930
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ttgaaaaatt tctgcatttc tcaaatgtgg acaaatacaa tagttttaaa gtattgtttt      1990

tctcagaagg gagataaaaa tgccgagtta gttaaagtgg gtcatgtgta aaatacgacc      2050

acttgatcgt gattatagtg ggcagtagag atgatgacaa gtcaatttcc atccagccgt      2110

gtatcctcat ggagaagctg cctgtctgaa tcaggatggc aagctggcag tctgggagga      2170

gcatgttttg cacagatgtt ttgtttggtc cacttggtga ggagtgcaga cagggctgcc      2230

tctctctagt cgggagagtc tgtgcattcc ctcgggccct gaccctagcc tcattcacat      2290

cacttgcccc tgtcgacacc taagtttgca ccctttgata gacaccatgt tcgatatctg      2350

aaaggctcag tgtcaggaga cagagactga gggagactga agacctgatt ctctgttccc      2410

tgcttgtttt ttaacttcaa actcagatga agccaatgga cctgctgaaa cacttgtctg      2470

tggaaactgg gtcaggtcgg gagatctact gaaatttggc ttttttcca tagccacgtg      2530

ccttctgttg ttgacagttc attcattacc aaagcctgtg tgtaactttg ccttgttctg      2590

tggccatctt cttgctcatg ttatttctcc tgggaatgag cagtttgact tctgttccca      2650

cgttcctcat tctatcagct ctagatggat tttgcctgca tagctggctt aatatgtctt      2710

tgtgtatggg tagtctgtag cctgagaata tttacctaaa aatgtctaaa cagccaccaa      2770

gaatgtttat aggggtatag gaatatagtt aacagagtgc taatctctcc tcaaatgtcc      2830

ttttggaatg cttcccccaa aattgggaag ttggtaggag cttttctttta ctttgaattt     2890

ctttacttgg acagaacgat tctgccttaa agacacgctt tgcagctctg ataaagaaca      2950

tccctgttta gtctcttgag ttttacaggc cacaaaatgt ccgtctcaga gggatctgtc      3010

tcagcttttc ttattttgc ttctctccgt tttcaaaatt aatcatcttg ttctctgtat       3070

aagaaaattt gagaagctgt ggacaattta atagtctgat ctggcaacag cgatttttgt      3130

ttggaaatat tttgtgtttt ctttgaggag gatataatta ctgatatcct aggatgtgaa      3190

attttgagt gacagtatgc acattttaaa gaaaattatg attaatctgt ataatgtttt       3250

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<212> DNA

<213> Homo sapiens

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<222> (61)...(1473)

<400> 58

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atg tct aga ctg gga gcc ctg ggt ggt gcc cgt gcc ggg ctg gga ctg		108
Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu		
1 5 10 15		

ttg ctg ggt acc gcc gcc ggc ctt gga ttc ctg tgc ctc ctt tac agc   156
Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser
           20   25   30

cag cga tgg aaa cgg acc cag cgt cat ggc cgc agc cag agc ctg ccc   204
Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro
           35   40   45

aac tcc ctg gac tat acg cag act tca gat ccc gga cgc cac gtg atg   252
Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met
       50   55   60

ctc ctg cgg gct gtc cca ggt ggg gct gga gat gcc tca gtg ctg ccc   300
Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro
65   70   75   80

agc ctt cca cgg gaa gga cag gag aag gtg ctg gac cgc ctg gac ttt   348
Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe

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                85                      90                      95
gtg ctg acc agc ctt gtg gcg ctg cgg cgg gag gtg gag gag ctg aga        396
Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg
                100                     105                     110
agc agc ctg cga ggg ctt gcg ggg gag att gtt ggg gag gtc cga tgc        444
Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys
                115                     120                     125
cac atg gaa gag aac cag aga gtg gct cgg cgg cga agg ttt ccg ttt        492
His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe
            130                     135                     140
gtc cgg gag agg agt gac tcc act ggc tcc agc tct gtc tac ttc acg        540
Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr
145                     150                     155                     160
gcc tcc tcg gga gcc acg ttc aca gat gct gag agt gaa ggg ggt tac        588
Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr
                165                     170                     175
aca aca gcc aat gcg gag tct gac aat gag cgg gac tct gac aaa gaa        636
Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu
                180                     185                     190
agt gag gac ggg gaa gat gaa gtg agc tgt gag act gtg aag atg ggg        684
Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly
                195                     200                     205
aga aag gat tct ctt gac ttg gag gaa gag gca gct tca ggt gcc tcc        732
Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser
            210                     215                     220
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agt gcc ctg gag gct gga ggt tcc tca ggc ttg gag gat gtg ctg ccc   780
Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro
225   230   235   240

ctc ctg cag cag gcc gac gag ctg cac agg ggt gat gag caa ggc aag   828
Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys
                245   250   255

cgg gag ggc ttc cag ctg ctg ctc aac aac aag ctg gtg tat gga agc   876
Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser
                260   265   270

cgg cag gac ttt ctc tgg cgc ctg gcc cga gcc tac agt gac atg tgt   924
Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys
            275   280   285

gag ctc act gag gag gtg agc gag aag aag tca tat gcc cta gat gga   972
Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly
290   295   300

aaa gaa gaa gca gag gct gct ctg gag aag ggg gat gag agt gct gac   1020
Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp
305   310   315   320

tgt cac ctg tgg tat gcg gtg ctt tgt ggt cag ctg gct gag cat gag   1068
Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu
                325   330   335

agc atc cag agg cgc atc cag agt ggc ttt agc ttc aag gag cat gtg   1116
Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val
                340   345   350

gac aaa gcc att gct ctc cag cca gaa aac ccc atg gct cac ttt ctt   1164

Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu

    355   360   365

ctt ggc agg tgg tgc tat cag gtc tct cac ctg agc tgg cta gaa aaa   1212

Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys

    370   375   380

aaa act gct aca gcc ttg ctt gaa agc cct ctc agt gcc act gtg gaa   1260

Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu

385   390   395   400

gat gcc ctc cag agc ttc cta aag gct gaa gaa cta cag cca gga ttt   1308

Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe

                    405   410   415

tcc aaa gca gga agg gta tat att tcc aag tgc tac aga gaa cta ggg   1356

Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly

                420   425   430

aaa aac tct gaa gct aga tgg tgg atg aag ttg gcc ctg gag ctg cca   1404

Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro

            435   440   445

gat gtc acg aag gag gat ttg gct atc cag aag gac ctg gaa gaa ctg   1452

Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu

        450   455   460

gaa gtc att tta cga gac taaccacgtt tcactggcct tcatgacttg   1500

Glu Val Ile Leu Arg Asp

465   470

atgccactat ttaaggtggg ggggcgggga ggcttttttc cttagacctt gctgagatca   1560

ggaaaccaca caaatctgtc tcctgggtct gactgctacc cactaccact ccccattagt   1620

taatttattc taacctctaa cctaatctag aattggggca gtactcatgg cttccgtttc   1680

tgttgttctc tcccttgagt aatctcttaa aaaaatcaag attcacacct gccccaggat   1740

tacacatggg tagagcctgc aagacctgag accttccaat tgctggtgag gtggatgaac   1800

ttcaaagcta taggaacaaa gcacataact tgtcacttta atcttttca ctgactaata   1860

ggactcagta catatagtct taagatcata ccttacctac caaggtaaaa agagggatca   1920

gagtggccca cagacattgc tttcttatca cctatcatgt gaattctacc tgtattcctg   1980

ggctggacca cttgataact tccagtgtcc tggcagcttt tggaatgaca gcagtggtat   2040

ggggtttatg atgctataaa acaatgtctg aaaagttgcc tagaatatat tttgttacaa   2100

acttgaaata aaccaaattt gatgtt   2126

<210> 59

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)... (805)

<400> 59

aatttggacc tgtgattcct tggttctcac aatcctctcc actctaagaa gcagggtgag   60

cccacaagga gca atg gag cag ggc agc ggc cgc ttg gag gac ttc cct   109
           Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro
           1   5   10

gtc aat gtg ttc tcc gtc act cct tac aca ccc agc acc gct gac atc   157
Val Asn Val Phe Ser Val Thr Pro Tyr Thr Pro Ser Thr Ala Asp Ile
15   20   25

```
cag gtg tcc gat gat gac aag gcg ggg gcc acc ttg ctc ttc tca ggc    205
Gln Val Ser Asp Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly
     30                  35                  40

atc ttt ctg gga ctg gtg ggg atc aca ttc act gtc atg ggc tgg atc    253
Ile Phe Leu Gly Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile
     45                  50                  55                  60

aaa tac caa ggt gtc tcc cac ttt gaa tgg acc cag ctc ctt ggg ccc    301
Lys Tyr Gln Gly Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro
                     65                  70                  75

gtc ctg ctg tca gtt ggg gtg aca ttc atc ctg att gct gtg tgc aag    349
Val Leu Leu Ser Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys
                     80                  85                  90

ttc aaa atg ctc tcc tgc cag ttg tgc aaa gaa agt gag gaa agg gtc    397
Phe Lys Met Leu Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val
                     95                 100                 105

ccg gac tcg gaa cag aca cca gga gga cca tca ttt gtt ttc act ggc    445
Pro Asp Ser Glu Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly
     110                 115                 120

atc aac caa ccc atc acc ttc cat ggg gcc act gtg gtg cag tac atc    493
Ile Asn Gln Pro Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile
125                 130                 135                 140

cct cct cct tat ggt tct cca gag cct atg ggg ata aat acc agc tac    541
Pro Pro Pro Tyr Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr
                     145                 150                 155

ctg cag tct gtg gtg agc ccc tgc ggc ctc ata acc tct gga ggg gca    589
```

Leu Gln Ser Val Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala
          160   165   170

gca gcc gcc atg tca agt cct cct caa tac tac acc atc tac cct caa   637
Ala Ala Ala Met Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln
          175   180   185

gat aac tct gca ttt gtg gtt gat gag ggc tgc ctt tct ttc acg gac   685
Asp Asn Ser Ala Phe Val Val Asp Glu Gly Cys Leu Ser Phe Thr Asp
          190   195   200

ggt gga aat cac agg ccc aat cct gat gtt gac cag cta gaa gag aca   733
Gly Gly Asn His Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr
205   210   215   220

cag ctg gaa gag gag gcc tgt gcc tgc ttc tct cct ccc cct tat gaa   781
Gln Leu Glu Glu Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu
                    225   230   235

gaa ata tac tct ctc cct cgc tagaggct attctgatat aataacacaa   830
Glu Ile Tyr Ser Leu Pro Arg
          240

tgctcagctc agggagcaag tgtttccgtc attgttacct gacaaccgtg gtgttctatg   890

ttgtaacctt cagaagttac agcagcgccc aggcagcctg acagagatca ttcaaggggg   950

gaaaggggaa gtgggaggtg caatttctca gattggtaaa aattaggctg ggctggggaa   1010

attctcctcc ggaacagttt caaattccct cgggtaagaa atctcctgta taaggttcag   1070

gagcaggaat ttactttttt catccaccac cctccccctt ctctgtagga aggcattggt   1130

ggctcaattt taaccccagc agccaatgga aaaatcacga cttctgagac tttgggagtt   1190

tccacagagg tgagagtcgg gtgggaagga agcagggaag agaaagcagg cccagctgga   1250

gatttcctgg tggctgtcct tggcccccaaa gcagactcac taatcccaaa caactcagct   1310

```
gccatctggc ctctctgagg actctgggta ccttaaagac tataaaacaa aacaaaacaa      1370

aaacatcaaa ccaatgaaat aaaataaatc atgtctcctg ctagaatagt attggatacc      1430

tgactaaatt acacaaaata gaccataata ggatagcact gtgaatacat ccttcccgat      1490

cactgagtca cagtgaccct tggctgctgc agttctcgtc tgcaaggttg aagcttgacg      1550

tgtgatgaac atgggtgggc tcttggtcca ccccaggctg gggcctgcgc caagcatgaa      1610

ctagctggga ccagtggctg acagaacaca ggacttccct aagtacccgt aggtccgtgg      1670

agcaagacag agcagagttg ccatgtcaac acatggggaa tgatatgata gaaacaatct      1730

ttatgactaa aagaaactca tcttcttcat taaaaaaact ttggtgtcct t              1781
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<210> 60

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (87)...(899)

<400> 60

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attgggcggc gtgatctcgc cgcggttccg cggccctgcc gccgccgccg ccagcagagc             60

gcaccgggcc gatcgggcga gtggcc atg gcg ggc gcc gag gac tgg ccg ggc             113
                                Met Ala Gly Ala Glu Asp Trp Pro Gly
                                1                   5

cag cag ctg gag ctg gac gag gac gag gcg tct tgt tgc cgc tgg ggc             161
Gln Gln Leu Glu Leu Asp Glu Asp Glu Ala Ser Cys Cys Arg Trp Gly
10              15                  20                  25

gcg cag cac gcc ggg gcc cgc gag ctg gct gcg ctc tac tcg cca ggc             209
```

```
Ala Gln His Ala Gly Ala Arg Glu Leu Ala Ala Leu Tyr Ser Pro Gly
                30                35                40

aag cgc ctc cag gag tgg tgc tct gtg atc ctg tgc ttc agc ctc atc     257
Lys Arg Leu Gln Glu Trp Cys Ser Val Ile Leu Cys Phe Ser Leu Ile
            45                50                55

gcc cac aac ctg gtc cat ctc ctg ctg ctg gcc cgc tgg gag gac aca     305
Ala His Asn Leu Val His Leu Leu Leu Leu Ala Arg Trp Glu Asp Thr
            60                65                70

ccc ctc gtc ata ctc ggt gtt gtt gca ggg gct ctc att gct gac ttc     353
Pro Leu Val Ile Leu Gly Val Val Ala Gly Ala Leu Ile Ala Asp Phe
        75                80                85

ttg tct ggc ctg gta cac tgg ggt gct gac aca tgg ggc tct gtg gag     401
Leu Ser Gly Leu Val His Trp Gly Ala Asp Thr Trp Gly Ser Val Glu
90                95                100                105

ctg ccc att gtg ggg aag gct ttc atc cga ccc ttc cgg gag cac cac     449
Leu Pro Ile Val Gly Lys Ala Phe Ile Arg Pro Phe Arg Glu His His
            110                115                120

att gac cca aca gct atc aca cgg cac gac ttc atc gag acc aac ggg     497
Ile Asp Pro Thr Ala Ile Thr Arg His Asp Phe Ile Glu Thr Asn Gly
            125                130                135

gac aac tgc ctg gtg aca ctg ctg ccg ctg cta aac atg gcc tac aag     545
Asp Asn Cys Leu Val Thr Leu Leu Pro Leu Leu Asn Met Ala Tyr Lys
            140                145                150

ttc cgc acc cac agc cct gaa gcc ctg gag cag cta tac ccc tgg gag     593
Phe Arg Thr His Ser Pro Glu Ala Leu Glu Gln Leu Tyr Pro Trp Glu
```

```
        155                   160                   165

tgc ttc gtc ttc tgc ctg atc atc ttc ggc acc ttc acc aac cag atc        641
Cys Phe Val Phe Cys Leu Ile Ile Phe Gly Thr Phe Thr Asn Gln Ile
170                   175                   180                   185

cac aag tgg tcg cac acg tac ttt ggg ctg cca cgc tgg gtc acc ctc        689
His Lys Trp Ser His Thr Tyr Phe Gly Leu Pro Arg Trp Val Thr Leu
                      190                   195                   200

ctg cag gac tgg cat gtc atc ctg cca cgt aaa cac cat cgc atc cac        737
Leu Gln Asp Trp His Val Ile Leu Pro Arg Lys His His Arg Ile His
                      205                   210                   215

cac gtc tca ccc cac gag acc tac ttc tgc atc acc aca ggc tgg ctc        785
His Val Ser Pro His Glu Thr Tyr Phe Cys Ile Thr Thr Gly Trp Leu
                      220                   225                   230

aac tac cct ctg gag aag ata ggc ttc tgg cga cgc ctg gag gac ctc        833
Asn Tyr Pro Leu Glu Lys Ile Gly Phe Trp Arg Arg Leu Glu Asp Leu
                      235                   240                   245

atc cag ggc ctg acg ggc gag aag cct cgg gca gat gac atg aaa tgg        881
Ile Gln Gly Leu Thr Gly Glu Lys Pro Arg Ala Asp Asp Met Lys Trp
250                   255                   260                   265

gcc cag aag atc aaa taac ttctccgagc ctgctacctg gttgccaacc            930
Ala Gln Lys Ile Lys
                      270

ttccctagcc cccaaaccga agccatctgc caaattccag cctctttgag ctggcccctc    990

cagatggaga ggacatctcc tgggctgggc ccaggtaccc cagcccaccc ctcatgacac    1050

agaatacttg agccactgat ttttcatttc tttttttttt ttttttcctcg gccctcctc    1110
```

```
agccacctga gttgctctat ctgcaagcct gactctgcca gcctcccctg gtagagagga   1170

ggtttaccca ctccctgcac gcctgccgtc cctgccccgc tgggcagccc ttcagtgtgg   1230

ctggcgttgg ggccagtgag ttgcctcttt ccctccttgt ctggccccag tggtctgggg   1290

agcccccagg cacacctaag cgtcgtggag cattgttctg ccacagccct gcatactgac   1350

cccgggaggc tgggcaggtg gacagcccca gccaccacct tcagcctagc ctgtccccca   1410

aggatggtga agctcagcag gggtctgagg gtagccggcc agaagaggct ggaacctcct   1470

gctcaagtct agacccctac ttctctgctg cccccaccct gccagagctg atgtttccaa   1530

taccaagatg tcttcacagg gcacagcccc tgcagagcat cttggtcatt tggaagagga   1590

cacggtatcc cctctggcca gagtatgtca gagaaggaag agtagggctt ttttgttttg   1650

tttttttta aaggtgcttg cttgtttaat gtaaataata gaaagcctta atatcttttc   1710

tgtaacacgg agtaatattt taatgtcatg ttttggatgt acataatata tttataacaa   1770

agcagcaaga gtctactt                                                 1788
```

<210> 61

<211> 389

<212> PRT

<213> Homo sapiens

<400> 61

Met Asp Arg Gly Glu Lys Ile Gln Leu Lys Arg Val Phe Gly Tyr Trp
1   5   10   15

Trp Gly Thr Ser Phe Leu Leu Ile Asn Ile Ile Gly Ala Gly Ile Phe
                20   25   30

Val Ser Pro Lys Gly Val Leu Ala Tyr Ser Cys Met Asn Val Gly Val
            35   40   45

Ser Leu Cys Val Trp Ala Gly Cys Ala Ile Leu Ala Met Thr Ser Thr

```
        50                  55                  60
Leu Cys Ser Ala Glu Ile Ser Ile Ser Phe Pro Cys Ser Gly Ala Gln

    65              70              75              80
Tyr Tyr Phe Leu Lys Arg Tyr Phe Gly Ser Thr Val Ala Phe Leu Asn

            85              90              95
Leu Trp Thr Ser Leu Phe Leu Gly Ser Gly Val Val Ala Gly Gln Ala

            100             105             110
Leu Leu Leu Ala Glu Tyr Ser Ile Gln Pro Phe Phe Pro Ser Cys Ser

            115             120             125
Val Pro Lys Leu Pro Lys Lys Cys Leu Ala Leu Ala Met Leu Trp Ile

            130             135             140
Val Gly Ile Leu Thr Ser Arg Gly Val Lys Glu Val Thr Trp Leu Gln

145             150             155             160
Ile Ala Ser Ser Val Leu Lys Val Ser Ile Leu Ser Phe Ile Ser Leu

                165             170             175
Thr Gly Val Val Phe Leu Ile Arg Gly Lys Lys Glu Asn Val Glu Arg

            180             185             190
Phe Gln Asn Ala Phe Asp Ala Glu Leu Pro Asp Ile Ser His Leu Ile

            195             200             205
Gln Ala Ile Phe Gln Gly Tyr Phe Ala Tyr Ser Gly Glu Leu Lys Lys

            210             215             220
Pro Arg Thr Thr Ile Pro Lys Cys Ile Phe Thr Ala Leu Pro Leu Val

225             230             235             240
Thr Val Val Tyr Leu Leu Val Asn Ile Ser Tyr Leu Thr Val Leu Thr

            245             250             255
```

Pro Arg Glu Ile Leu Ser Ser Asp Ala Val Ala Ile Thr Trp Ala Asp

            260   265   270

Arg Ala Phe Pro Ser Leu Ala Trp Ile Met Pro Phe Ala Ile Ser Thr

            275   280   285

Ser Leu Phe Ser Asn Leu Leu Ile Ser Ile Phe Lys Ser Ser Arg Pro

    290   295   300

Ile Tyr Leu Ala Ser Gln Glu Gly Gln Leu Pro Leu Leu Phe Asn Thr

305   310   315   320

Leu Asn Ser His Ser Ser Pro Phe Thr Ala Val Leu Leu Leu Val Thr

                325   330   335

Leu Gly Ser Leu Ala Ile Ile Leu Thr Ser Leu Ile Asp Leu Ile Asn

            340   345   350

Tyr Ile Phe Phe Thr Gly Ser Leu Trp Ser Ile Leu Leu Met Ile Gly

            355   360   365

Ile Leu Arg Arg Arg Tyr Gln Glu Pro Asn Leu Ser Ile Pro Tyr Lys

            370   375   380

Val Lys Leu Asp Phe

385

<210> 62

<211> 348

<212> PRT

<213> Homo sapiens

<400> 62

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg

```
        1                5               10              15
Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu Leu

                20              25              30
Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly Gln Thr Phe

        35              40              45
Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro Tyr Gln Gly Val

      50              55              60
Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met Gly Asn Ala Met Val

    65              70              75              80
Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp Met Gln Ser Lys Gln Gly

                85              90              95
Ala Leu Trp Asn Arg Val Pro Cys Phe Leu Arg Asp Trp Glu Leu Gln

            100             105             110
Val His Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp

          115             120             125
Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg Met Gln Pro Gly Pro Val

        130             135             140
Phe Gly Asn Met Asp Lys Phe Val Gly Leu Gly Val Phe Val Asp Thr

145             150             155             160
Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser

                165             170             175
Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly

              180             185             190
Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His

            195             200             205
```

Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile
        210   215   220

Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val
225   230   235   240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser Ile
                245   250   255

Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys Leu Phe
                260   265   270

Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu His Arg Asp
            275   280   285

Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro Glu Met Thr Ala
        290   295   300

Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile Val Phe Phe
305   310   315   320

Ser Leu Val Phe Ser Val Phe Ala Ile Val Ile Gly Ile Ile Leu Tyr
                325   330   335

Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg Phe Tyr
        340   345

<210> 63

<211> 261

<212> PRT

<213> Homo sapiens

<400> 63

Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys

```
          1                    5                   10                  15
Ser Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val

                  20                  25                  30
Val Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu

                  35                  40                  45
Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr

          50                  55                  60
Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe

      65                  70                  75                  80
Leu Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg

                  85                  90                  95
Lys Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu

                  100                 105                 110
Pro Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr

          115                 120                 125
Gln Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro

          130                 135                 140
Asp Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr

      145                 150                 155                 160
Ile Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Gly Thr Glu Gly Gly

                  165                 170                 175
Lys Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile

                  180                 185                 190
Leu Pro Val Val Ile Ala Leu Ile Val Ile Thr Leu Ser Val Phe Val

          195                 200                 205
```

Leu Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro
        210   215   220

Glu Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu
225   230   235   240

Leu Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln
                    245   250   255

Gly Lys Thr Lys Asn
            260

<210> 64

<211> 222

<212> PRT

<213> Homo sapiens

<400> 64

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu
  1   5   10   15

Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg
                20   25   30

Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr
            35   40   45

Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg
        50   55   60

Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys Asn Val Thr Gln Arg
65   70   75   80

Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His Thr Leu

                    85   90   95

Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn Arg Ile

                    100   105   110

Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Glu Phe Leu Lys Ile

                    115   120   125

Pro Ser Thr Leu Ala Pro Pro Met Asp Pro Ser Val Pro Ile Trp Ile

               130   135   140

Ile Ile Phe Gly Val Ile Phe Cys Ile Ile Ile Val Ala Ile Ala Leu

145   150   155   160

Leu Ile Leu Ser Gly Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro

                    165   170   175

Ser Glu Val Asp Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile

                    180   185   190

Glu Asn Gly Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly His Ile

                    195   200   205

Asn Asp Ala Phe Met Thr Glu Asp Glu Arg Leu Thr Pro Leu

          210   215   220

<210> 65

<211> 183

<212> PRT

<213> Homo sapiens

<400> 65

Met Gly Val Arg Val His Val Val Ala Ala Ser Ala Leu Leu Tyr Phe

     1   5   10   15

Ile Leu Leu Ser Gly Thr Arg Cys Glu Glu Asn Cys Gly Asn Pro Glu
              20   25   30

His Cys Leu Thr Thr Asp Trp Val His Leu Trp Tyr Ile Trp Leu Leu
              35   40   45

Val Val Ile Gly Ala Leu Leu Leu Leu Cys Gly Leu Thr Ser Leu Cys
              50   55   60

Phe Arg Cys Cys Cys Leu Ser Arg Gln Gln Asn Gly Glu Asp Gly Gly
65   70   75   80

Pro Pro Pro Cys Glu Val Thr Val Ile Ala Phe Asp His Asp Ser Thr
                  85   90   95

Leu Gln Ser Thr Ile Thr Ser Leu Gln Ser Val Phe Gly Pro Ala Ala
                  100   105   110

Arg Arg Ile Leu Ala Val Ala His Ser His Ser Ser Leu Gly Gln Leu
              115   120   125

Pro Ser Ser Leu Asp Thr Leu Pro Gly Tyr Glu Glu Ala Leu His Met
    130   135   140

Ser Arg Phe Thr Val Ala Met Cys Gly Gln Lys Ala Pro Asp Leu Pro
145   150   155   160

Pro Val Pro Glu Glu Lys Gln Leu Pro Pro Thr Glu Lys Glu Ser Thr
                  165   170   175

Arg Ile Val Asp Ser Trp Asn
              180

<210> 66

<211> 262

146/307

<212> PRT

<213> Homo sapiens

<400> 66

Met Gly Lys Thr Phe Ser Gln Leu Gly Ser Trp Arg Glu Asp Glu Asn
1   5   10   15

Lys Ser Ile Leu Ser Ser Lys Pro Ala Ile Gly Ser Lys Ala Val Asn
        20   25   30

Tyr Ser Ser Thr Gly Ser Ser Lys Ser Phe Cys Ser Cys Val Pro Cys
        35   40   45

Glu Gly Thr Ala Asp Ala Ser Phe Val Thr Cys Pro Thr Cys Gln Gly
       50   55   60

Ser Gly Lys Ile Pro Gln Glu Leu Glu Lys Gln Leu Val Ala Leu Ile
65   70   75   80

Pro Tyr Gly Asp Gln Arg Leu Lys Pro Lys His Thr Lys Leu Phe Val
         85   90   95

Phe Leu Ala Val Leu Ile Cys Leu Val Thr Ser Ser Phe Ile Val Phe
        100   105   110

Phe Leu Phe Pro Arg Ser Val Ile Val Gln Pro Ala Gly Leu Asn Ser
        115   120   125

Ser Thr Val Ala Phe Asp Glu Ala Asp Ile Tyr Leu Asn Ile Thr Asn
        130   135   140

Ile Leu Asn Ile Ser Asn Gly Asn Tyr Tyr Pro Ile Met Val Thr Gln
145   150   155   160

Leu Thr Leu Glu Val Leu His Leu Ser Leu Val Val Gly Gln Val Ser
        165   170   175

Asn Asn Leu Leu Leu His Ile Gly Pro Leu Ala Ser Glu Gln Met Phe
                180   185   190

Tyr Ala Val Ala Thr Lys Ile Arg Asp Glu Asn Thr Tyr Lys Ile Cys
            195   200   205

Thr Trp Leu Glu Ile Lys Val His His Val Leu Leu His Ile Gln Gly
        210   215   220

Thr Leu Thr Cys Ser Tyr Leu Ser His Ser Glu Gln Leu Val Phe Gln
225   230   235   240

Ser Tyr Glu Tyr Val Asp Cys Arg Gly Asn Ala Ser Val Pro His Gln
                245   250   255

Leu Thr Pro His Pro Pro
                260

<210> 67

<211> 168

<212> PRT

<213> Homo sapiens

<400> 67

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser
1   5   10   15

Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Lys Asp Ala Pro
            20   25   30

Ser Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile
        35   40   45

Thr Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys

```
        50                  55                  60
Leu Pro Leu Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser
        65                  70                  75                  80
Asn Arg Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly
                    85                  90                  95
Ile Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro
                    100                 105                 110
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro
                    115                 120                 125
Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser
        130                 135                 140
Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro
145                 150                 155                 160
Asp Ser Pro Asn Phe Glu Val Ile
            165
```

<210> 68

<211> 243

<212> PRT

<213> Homo sapiens

<400> 68

```
Met Ser Ser Gly Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val
    1                   5                   10                  15
Leu Leu Gly Val Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro Gly
            20                  25                  30
```

Ala Lys Arg Ser Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp

35   40   45

Gln Gln Ser Phe Thr Gly Ser Arg Thr Tyr Ser Leu Val Gly Gln Ala

50   55   60

Trp Pro Gly Pro Leu Ala Asp Met Ala Pro Thr Arg Lys Asp Lys Leu

65   70   75   80

Leu Gln Phe Tyr Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr Gln

85   90   95

Asn Phe Ser Lys Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile Asp

100   105   110

Pro Ile Ala Met Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro Pro

115   120   125

Glu Asp Asp Asp Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln

130   135   140

Lys Thr Thr Glu Thr Gly Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys

145   150   155   160

Arg Gly Asp Leu Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser

165   170   175

Gly Leu Cys Pro Ser Ala Ser Pro Glu Glu Asp Glu Glu Ser Glu Asp

180   185   190

Tyr Gln Asn Ser Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val

195   200   205

Met Gly Gln Leu Gln Arg Glu Ala Ser Pro Gly Pro Val Gly Ser Pro

210   215   220

Asp Glu Glu Asp Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala

225   230   235   240

Thr Glu Ala

<210> 69

<211> 428

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Ser Leu Cys Pro Gly Ala Trp Leu Arg Lys Pro Tyr Tyr

1   5   10   15

Leu Gln Ala Arg Phe Ser Tyr Val Arg Met Lys Tyr Leu Phe Phe Ser

          20   25   30

Trp Leu Val Val Phe Val Gly Ser Trp Ile Ile Tyr Val Gln Tyr Ser

          35   40   45

Thr Tyr Thr Glu Leu Cys Arg Gly Lys Asp Cys Lys Lys Ile Ile Cys

          50   55   60

Asp Lys Tyr Lys Thr Gly Val Ile Asp Gly Pro Ala Cys Asn Ser Leu

65   70   75   80

Cys Val Thr Glu Thr Leu Tyr Phe Gly Lys Cys Leu Ser Thr Lys Pro

              85   90   95

Asn Asn Gln Met Tyr Leu Gly Ile Trp Asp Asn Leu Pro Gly Val Val

            100   105   110

Lys Cys Gln Met Glu Gln Ala Leu His Leu Asp Phe Gly Thr Glu Leu

            115   120   125

Glu Pro Arg Lys Glu Ile Val Leu Phe Asp Lys Pro Thr Arg Gly Thr
        130   135   140

Thr Val Gln Lys Phe Lys Glu Met Val Tyr Ser Leu Phe Lys Ala Lys
145   150   155   160

Leu Gly Asp Gln Gly Asn Leu Ser Glu Leu Val Asn Leu Ile Leu Thr
                165   170   175

Val Ala Asp Gly Asp Lys Asp Gly Gln Val Ser Leu Gly Glu Ala Lys
            180   185   190

Ser Ala Trp Ala Leu Leu Gln Leu Asn Glu Phe Leu Leu Met Val Ile
            195   200   205

Leu Gln Asp Lys Glu His Thr Pro Lys Leu Met Gly Phe Cys Gly Asp
        210   215   220

Leu Tyr Val Met Glu Ser Val Glu Tyr Thr Ser Leu Tyr Gly Ile Ser
225   230   235   240

Leu Pro Trp Val Ile Glu Leu Phe Ile Pro Ser Gly Phe Arg Arg Ser
                245   250   255

Met Asp Gln Leu Phe Thr Pro Ser Trp Pro Arg Lys Ala Lys Ile Ala
            260   265   270

Ile Gly Leu Leu Glu Phe Val Glu Asp Val Phe His Gly Pro Tyr Gly
            275   280   285

Asn Phe Leu Met Cys Asp Thr Ser Ala Lys Asn Leu Gly Tyr Asn Asp
        290   295   300

Lys Tyr Asp Leu Lys Met Val Asp Met Arg Lys Ile Val Pro Glu Thr
305   310   315   320

Asn Leu Lys Glu Leu Ile Lys Asp Arg His Cys Glu Ser Asp Leu Asp

```
            325                 330                 335
Cys Val Tyr Gly Thr Asp Cys Arg Thr Ser Cys Asp Gln Ser Thr Met
                340                 345                 350
Lys Cys Thr Ser Glu Val Ile Gln Pro Asn Leu Ala Lys Ala Cys Gln
            355                 360                 365
Leu Leu Lys Asp Tyr Leu Leu Arg Gly Ala Pro Ser Glu Ile Arg Glu
            370                 375                 380
Glu Leu Glu Lys Gln Leu Tyr Ser Cys Ile Ala Leu Lys Val Thr Ala
385                 390                 395                 400
Asn Gln Met Glu Met Glu His Ser Leu Ile Leu Asn Asn Leu Lys Thr
                405                 410                 415
Leu Leu Trp Lys Lys Ile Ser Tyr Thr Asn Asp Ser
                420                 425
```

<210> 70

<211> 283

<212> PRT

<213> Homo sapiens

<400> 70

```
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
  1                 5                 10                 15
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
                20                 25                 30
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
            35                 40                 45
```

Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys

      50   55   60

Ser Leu Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser

65   70   75   80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly

                  85   90   95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala

                  100   105   110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln

                  115   120   125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile

      130   135   140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala

145   150   155   160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln

                  165   170   175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly

                  180   185   190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val

                  195   200   205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys

      210   215   220

Leu Pro Gln Gln Thr Ala Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr

225   230   235   240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Asn Leu Gln

```
                  245                   250                   255
Met Thr Ala Ala Ser Arg Cys Pro Arg Arg Phe Ser Gly Thr Cys Gly

                  260                   265                   270
Arg Arg Lys Arg Lys Arg Leu Leu Trp Ala Ala

                  275                   280
```

<210> 71

<211> 1167

<212> DNA

<213> Homo sapiens

<400> 71

```
atggatagag gggagaaaat acagctcaag agagtgtttg gatattggtg gggcacaagt      60

ttttttgctta ttaatatcat tggtgcagga attttttgtgt ccccccaaagg tgtgttggca    120

tactcttgca tgaacgtggg agtctccctg tgcgtttggg ctggctgtgc catactggcc      180

atgacatcaa ctctttgctc tgcagagata agtataagct tcccatgcag tggagctcaa      240

tactattttc tcaagagata ctttggctcc acggttgctt ttttgaatct ctggacatcc      300

ttgtttctgg ggtcaggggt agttgctggc caagctctgc tccttgctga gtacagcatc      360

cagcctttt  ttcccagctg ctctgtccca aagctgccta agaaatgtct ggcattggcc      420

atgttgtgga ttgtaggaat tctgacttct cgtggtgtga agaagtgac  ttggcttcag      480

atagctagct cagtgctgaa agtgtccata cttagcttca tttccctaac tggagtagtg      540

ttcctgataa gagggaaaaa ggagaatgta gaacgatttc agaatgcttt tgatgctgaa      600

cttccagata tctctcacct tatacaagcc atcttccaag gatattttgc atattcaggg      660

gagctgaaga agcccagaac aacaattccc aaatgcatat ttactgcgtt acctctggtg      720

actgtagttt atttactggt taacatttcc tatctgactg ttctgacacc cagggaaatt      780

ctctcttcag atgctgtagc tatcacatgg gctgatcgag cttttcccctc attagcatgg      840
```

```
attatgcctt ttgctatttc tacctcatta tttagcaacc ttctgatttc tatatttaaa    900

tcttcgagac caatatatct tgcaagccaa gagggccagc tgcctttgct atttaataca    960

cttaatagtc actcttctcc atttacagct gtgctactac ttgtcacttt gggatccctt    1020

gcaattatct taacaagtct aattgatttg ataaactata ttttttcac gggttcatta     1080

tggtctatat tattaatgat aggaatacta aggcggagat accaggaacc caatctatct    1140

ataccttata aggtaaaatt ggatttc                                        1167
```

<210> 72

<211> 1044

<212> DNA

<213> Homo sapiens

<400> 72

```
atggcggcga ctctgggacc ccttgggtcg tggcagcagt ggcggcgatg tttgtcggct      60

cgggatgggt ccaggatgtt actccttctt cttttgttgg ggtctgggca ggggccacag     120

caagtcgggg cgggtcaaac gttcgagtac ttgaaacggg agcactcgct gtcgaagccc     180

taccagggtg tgggcacagg cagttcctca ctgtggaatc tgatgggcaa tgccatggtg     240

atgacccagt atatccgcct taccccagat atgcaaagta aacagggtgc cttgtggaac     300

cgggtgccat gtttcctgag agactgggag ttgcaggtgc acttcaaaat ccatggacaa     360

ggaaagaaga atctgcatgg ggatggcttg gcaatctggt acacaaagga tcggatgcag     420

ccagggcctg tgtttggaaa catggacaaa tttgtggggc tgggagtatt tgtagacacc     480

taccccaatg aggagaagca gcaagagcgg gtattcccct acatctcagc catggtgaac     540

aacggctccc tcagctatga tcatgagcgg gatgggcggc tacagagct gggaggctgc     600

acagccattg tccgcaatct tcattacgac accttcctgg tgattcgcta cgtcaagagg     660

catttgacga taatgatgga tattgatggc aagcatgagt ggagggactg cattgaagtg     720

cccggagtcc gcctgccccg cggctactac ttcggcacct cctccatcac tggggatctc     780
```

```
tcagataatc atgatgtcat ttccttgaag ttgtttgaac tgacagtgga gagaacccca    840

gaagaggaaa agctccatcg agatgtgttc ttgccctcag tggacaatat gaagctgcct    900

gagatgacag ctccactgcc gcccctgagt ggcctggccc tcttcctcat cgtctttttc    960

tccctggtgt tttctgtatt tgccatagtc attggtatca tactctacaa caaatggcag   1020

gaacagagcc gaaagcgctt ctac                                          1044
```

<210> 73

<211> 783

<212> DNA

<213> Homo sapiens

<400> 73

```
atggaactgc ttcaagtgac cattcttttt cttctgccca gtatttgcag cagtaacagc     60

acaggtgttt tagaggcagc taataattca cttgttgtta ctacaacaaa accatctata    120

acaacaccaa acacagaatc attacagaaa aatgttgtca caccaacaac tggaacaact    180

cctaaaggaa caatcaccaa tgaattactt aaaatgtctc tgatgtcaac agctactttt    240

ttaacaagta aagatgaagg attgaaagcc acaaccactg atgtcaggaa gaatgactcc    300

atcatttcaa acgtaacagt aacaagtgtt acacttccaa atgctgtttc aacattacaa    360

agttccaaac ccaagactga aactcagagt tcaattaaaa caacagaaat accaggtagt    420

gttctacaac cagatgcatc accttctaaa actggtacat taacctcaat accagttaca    480

attccagaaa acacctcaca gtctcaagta ataggcactg agggtggaaa aaatgcaagc    540

acttcagcaa ccagccggtc ttattccagt attattttgc cggtggttat tgctttgatt    600

gtaataacac tttcagtatt tgttctggtg ggtttgtacc gaatgtgctg gaaggcagat    660

ccgggcacac cagaaatgg aaatgatcaa cctcagtctg ataaagagag cgtgaagctt    720

cttaccgtta agacaatttc tcatgagtct ggtgagcact ctgcacaagg aaaaaccaag    780

aac                                                                  783
```

<210> 74

<211> 666

<212> DNA

<213> Homo sapiens

<400> 74

```
atgttgtggc tgctcttttt tctggtgact gccattcatg ctgaactctg tcaaccaggt       60

gcagaaaatg cttttaaagt gagacttagt atcagaacag ctctgggaga taaagcatat      120

gcctgggata ccaatgaaga atacctcttc aaagcgatgg tagctttctc catgagaaaa      180

gttcccaaca gagaagcaac agaaatttcc catgtcctac tttgcaatgt aacccagagg      240

gtatcattct ggtttgtggt tacagaccct tcaaaaaatc acacccttcc tgctgttgag      300

gtgcaatcag ccataagaat gaacaagaac cggatcaaca atgccttctt tctaaatgac      360

caaactctgg aattttttaaa aatcccttcc acacttgcac cacccatgga cccatctgtg      420

cccatctgga ttattatatt tggtgtgata ttttgcatca tcatagttgc aattgcacta      480

ctgattttat cagggatctg gcaacgtaga agaaagaaca agaaccatc tgaagtggat      540

gacgctgaag ataagtgtga aaacatgatc acaattgaaa atggcatccc ctctgatccc      600

ctggacatga agggagggca tattaatgat gccttcatga cagaggatga gaggctcacc      660

cctctc                                                                  666
```

<210> 75

<211> 549

<212> DNA

<213> Homo sapiens

<400> 75

```
atgggagtcc gagttcatgt cgtggcggcc tcagccctgc tgtatttcat cctgctttct       60
```

```
gggacgagat gtgaggaaaa ctgtggtaat cctgaacatt gcctgaccac agactgggta    120

catctctggt atatatggtt gctagtggta attggcgcgc tgcttctcct gtgtggcctg    180

acgtccctgt gcttccgctg ctgctgtctg agccgccagc aaaatgggga agatgggggc    240

ccaccaccct gtgaagtgac cgtcattgct ttcgatcacg acagcactct ccagagcact    300

atcacatctc tgcagtcggt gtttggccct gcagctcgga ggatcctggc tgtggctcac    360

tcccacagct ccctgggcca gctgccctcc tctttggaca ccctcccagg gtatgaagaa    420

gctcttcaca tgagtcgctt cacagtagcc atgtgcgggc agaaagcacc tgatctaccc    480

ccagtacctg aagaaaagca gctgcctcca acagagaagg agtcgactcg aatagttgac    540

tcttggaac                                                           549
```

```
<210> 76

<211> 786

<212> DNA

<213> Homo sapiens

<400> 76

atgggtaaga cgttttccca gctgggctct tggcgggagg atgagaacaa gtcaatcctg     60

tcctccaaac cagccattgg cagcaaggct gtcaactact ccagcaccgg tagcagcaag    120

tcttttttgtt cctgtgtgcc ttgtgaagga actgctgatg ccagcttcgt gacttgtccc    180

acctgccagg gcagtggcaa gattccccaa gagctggaga agcagttggt ggctctcatt    240

ccctatgggg accagaggct gaagcccaag cacacgaagc tctttgtgtt cctggccgtg    300

ctcatctgcc tggtgacctc ctccttcatc gtcttttttcc tgtttccccg gtccgtcatt    360

gtgcagcctg caggcctcaa ctcctccaca gtggcctttg atgaggctga tatctacctc    420

aacataacga atatcttaaa catctccaat ggcaactact accccattat ggtgacacag    480

ctgaccctcg aggttctgca cctgtccctc gtggtggggc aggtttccaa caaccttctc    540

ctacacattg gcccctttggc cagtgaacag atgtttttacg cagtagctac caagatacgg    600
```

```
gatgaaaaca catacaaaat ctgtacctgg ctggaaatca aagtccacca tgtgcttttg     660

cacatccagg gcaccctgac ctgttcatac ctgagccatt cagagcagct ggtctttcag     720

agctatgaat atgtggactg ccgaggaaac gcatctgtgc cccaccagct gacccctcac     780

ccacca                                                                786
```

<210> 77

<211> 504

<212> DNA

<213> Homo sapiens

<400> 77

```
atgggcgtcc ccacggccct ggaggccggc agctggcgct ggggatccct gctcttcgct     60

ctcttcctgg ctgcgtccct aggcaaagat gcaccatcca actgtgtggt gtacccatcc     120

tcctcccagg agagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta     180

ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca ggcagcctcc     240

aaccgccgtg cccaggagct ggtgcggatg gacagcaaca ttcaagggat tgaaaacccc     300

ggctttgaag cctcaccacc tgcccagggg atacccgagg ccaaagtcag gcaccccctg      360

tcctatgtgg cccagcggca gccttctgag tctgggcggc atctgctttc ggagcccagc     420

acccccctgt ctcctccagg ccccggagac gtcttcttcc catccctgga ccctgtccct     480

gactctccaa actttgaggt catc                                            504
```

<210> 78

<211> 729

<212> DNA

<213> Homo sapiens

<400> 78

```
atgagctcgg ggactgaact gctgtggccc ggagcagcgc tgctggtgct gttgggggtg      60

gcagccagtc tgtgtgtgcg ctgctcacgc ccaggtgcaa agaggtcaga gaaaatctac     120

cagcagagaa gtctgcgtga ggaccaacag agctttacgg ggtcccggac ctactccttg     180

gtcgggcagg catggccagg acccctggcg gacatggcac ccacaaggaa ggacaagctg     240

ttgcaattct accccagcct ggaggatcca gcatcttcca ggtaccagaa cttcagcaaa     300

ggaagcagac acgggtcgga ggaagcctac atagacccca ttgccatgga gtattacaac     360

tgggggcggt tctcgaagcc cccagaagat gatgatgcca attcctacga gaatgtgctc     420

atttgcaagc agaaaaccac agagacaggt gcccagcagg agggcatagg tggcctctgc     480

agaggggacc tcagcctgtc actggccctg aagactggcc ccacttctgg tctctgtccc     540

tctgcctccc cggaagaaga tgaggaatct gaggattatc agaactcagc atccatccat     600

cagtggcgcg agtccaggaa ggtcatgggg caactccaga gagaagcatc ccctggcccg     660

gtgggaagcc cagacgagga ggacggggaa ccggattacg tgaatgggga ggtggcagcc     720

acagaagcc                                                            729
```

```
<210> 79

<211> 1284

<212> DNA

<213> Homo sapiens

<400> 79

atggcgagga gtctctgtcc gggggcctgg ctaaggaaac cctattacct ccaggctcgc      60

ttctcatatg tgcggatgaa atatcttttc ttttcctggt tagtggtttt tgttggaagc     120

tggattatat atgtgcagta ttctacctat acagaattat gcagaggaaa ggactgtaag     180

aaaataatat gtgacaagta caagactgga gttattgatg ggcctgcatg taacagcctt     240

tgtgttacag aaactcttta ctttggaaaa tgtttatcca ccaagcccaa caatcagatg     300

tatttaggga tttgggataa ctaccaggt gttgtgaaat gtcaaatgga acaagcgctt     360
```

```
catcttgatt ttggaactga attggaacca agaaaagaaa tagtgctatt tgataagcca    420

actagaggaa ctactgtaca aaaatttaaa gaaatggtct atagtctctt taaggcaaaa    480

ttgggtgacc aaggaaacct ctctgaactg gttaatctca tcttgacggt ggctgatgga    540

gacaaagatg ccaggtttc cttgggagaa gcaaagtcgg catgggcact tcttcaactg    600

aatgaatttc ttctcatggt gatacttcaa gataaagaac atacccccaa attaatggga    660

ttctgtggtg acctctatgt gatggaaagt gttgaatata cctctcttta tggaataagc    720

cttccttggg tcattgaact ttttattcca tctgggttca gaagaagcat ggatcagctg    780

ttcacaccat catggccaag aaaggccaaa atagccatag gacttctaga atttgtggaa    840

gatgttttcc atggccccta cggaaatttc ctcatgtgcg atactagtgc caaaaaccta    900

ggatataatg ataagtatga tttgaaaatg gtggatatga gaaaaattgt gccagagaca    960

aacctgaaag aacttattaa ggatcgtcac tgtgagtctg atttggactg tgtctatggc   1020

acagattgta gaactagctg tgatcagagt acaatgaagt gtacttcaga agtgatacaa   1080

ccaaacttgg caaaagcttg tcagttactc aaagactacc tactgcgtgg tgctccaagt   1140

gaaattcgtg aagaattaga aaagcagctt tattcttgta ttgctctcaa agtcacagca   1200

aatcaaatgg aaatggaaca ttctttgata ctaaataacc taaaaacatt attgtggaag   1260

aaaatttcct acactaatga ctct                                          1284
```

<210> 80

<211> 849

<212> DNA

<213> Homo sapiens

<400> 80

```
atgccccact ccagcctgca tccatccatc ccgtgtccca ggggtcacgg ggcccagaag    60

gcagccttgg ttctgctgag tgcctgcctg gtgacccttt gggggctagg agagccacca   120

gagcacactc tccggtacct ggtgctccac ctagcctccc tgcagctggg actgctgtta   180
```

```
aacggggtct gcagcctggc tgaggagctg caccacatcc actccaggta ccggggcagc    240

tactggagga ctgtgcgggc ctgcctgggc tgccccctcc gccgtggggc cctgttgctg    300

ctgtccatct atttctacta ctccctccca aatgcggtcg gcccgccctt cacttggatg    360

cttgccctcc tgggcctctc gcaggcactg aacatcctcc tgggcctcaa gggcctggcc    420

ccagctgaga tctctgcagt gtgtgaaaaa gggaatttca cgtggcccca tgggctggca    480

tggtcatatt acatcggata tctgcggctg atcctgccag agctccaggc ccggattcga    540

acttacaatc agcattacaa caacctgcta cggggtgcag tgagccagcg gctgtatatt    600

ctcctcccat tggactgtgg ggtgcctgat aacctgagta tggctgaccc caacattcgc    660

ttcctggata aactgcccca gcagaccgct gaccgtgctg gcatcaagga tcgggtttac    720

agcaacagca tctatgagct tctggagaac gggcagcgga acctgcagat gacagcagct    780

tctcgctgtc ccaggaggtt ctccggcacc tgcggcagga ggaaaaggaa gaggttactg    840

tgggcagct                                                            849
```

<210> 81

<211> 1376

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (100)...(1269)

<400> 81

```
atttttattt caggaatcca tcaacatcct ttgcagctac ataggcagga aaatctagaa    60

attgtaattt atatagaatt ttaaaactct tcaattaca atg gat aga ggg gag       114
                                              Met Asp Arg Gly Glu
                                                1               5
```

aaa ata cag ctc aag aga gtg ttt gga tat tgg tgg ggc aca agt ttt   162
Lys Ile Gln Leu Lys Arg Val Phe Gly Tyr Trp Trp Gly Thr Ser Phe
                    10   15   20

ttg ctt att aat atc att ggt gca gga att ttt gtg tcc ccc aaa ggt   210
Leu Leu Ile Asn Ile Ile Gly Ala Gly Ile Phe Val Ser Pro Lys Gly
                25   30   35

gtg ttg gca tac tct tgc atg aac gtg gga gtc tcc ctg tgc gtt tgg   258
Val Leu Ala Tyr Ser Cys Met Asn Val Gly Val Ser Leu Cys Val Trp
            40   45   50

gct ggc tgt gcc ata ctg gcc atg aca tca act ctt tgc tct gca gag   306
Ala Gly Cys Ala Ile Leu Ala Met Thr Ser Thr Leu Cys Ser Ala Glu
        55   60   65

ata agt ata agc ttc cca tgc agt gga gct caa tac tat ttt ctc aag   354
Ile Ser Ile Ser Phe Pro Cys Ser Gly Ala Gln Tyr Tyr Phe Leu Lys
70   75   80   85

aga tac ttt ggc tcc acg gtt gct ttt ttg aat ctc tgg aca tcc ttg   402
Arg Tyr Phe Gly Ser Thr Val Ala Phe Leu Asn Leu Trp Thr Ser Leu
                90   95   100

ttt ctg ggg tca ggg gta gtt gct ggc caa gct ctg ctc ctt gct gag   450
Phe Leu Gly Ser Gly Val Val Ala Gly Gln Ala Leu Leu Leu Ala Glu
                105   110   115

tac agc atc cag cct ttt ttt ccc agc tgc tct gtc cca aag ctg cct   498
Tyr Ser Ile Gln Pro Phe Phe Pro Ser Cys Ser Val Pro Lys Leu Pro
                120   125   130

aag aaa tgt ctg gca ttg gcc atg ttg tgg att gta gga att ctg act   546

Lys Lys Cys Leu Ala Leu Ala Met Leu Trp Ile Val Gly Ile Leu Thr
        135   140   145

tct cgt ggt gtg aaa gaa gtg act tgg ctt cag ata gct agc tca gtg   594
Ser Arg Gly Val Lys Glu Val Thr Trp Leu Gln Ile Ala Ser Ser Val
150   155   160   165

ctg aaa gtg tcc ata ctt agc ttc att tcc cta act gga gta gtg ttc   642
Leu Lys Val Ser Ile Leu Ser Phe Ile Ser Leu Thr Gly Val Val Phe
                170   175   180

ctg ata aga ggg aaa aag gag aat gta gaa cga ttt cag aat gct ttt   690
Leu Ile Arg Gly Lys Lys Glu Asn Val Glu Arg Phe Gln Asn Ala Phe
                185   190   195

gat gct gaa ctt cca gat atc tct cac ctt ata caa gcc atc ttc caa   738
Asp Ala Glu Leu Pro Asp Ile Ser His Leu Ile Gln Ala Ile Phe Gln
        200   205   210

gga tat ttt gca tat tca ggg gag ctg aag aag ccc aga aca aca att   786
Gly Tyr Phe Ala Tyr Ser Gly Glu Leu Lys Lys Pro Arg Thr Thr Ile
        215   220   225

ccc aaa tgc ata ttt act gcg tta cct ctg gtg act gta gtt tat tta   834
Pro Lys Cys Ile Phe Thr Ala Leu Pro Leu Val Thr Val Val Tyr Leu
230   235   240   245

ctg gtt aac att tcc tat ctg act gtt ctg aca ccc agg gaa att ctc   882
Leu Val Asn Ile Ser Tyr Leu Thr Val Leu Thr Pro Arg Glu Ile Leu
                250   255   260

tct tca gat gct gta gct atc aca tgg gct gat cga gct ttt ccc tca   930
Ser Ser Asp Ala Val Ala Ile Thr Trp Ala Asp Arg Ala Phe Pro Ser

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              265                270                275
tta gca tgg att atg cct ttt gct att tct acc tca tta ttt agc aac    978
Leu Ala Trp Ile Met Pro Phe Ala Ile Ser Thr Ser Leu Phe Ser Asn
              280                285                290
ctt ctg att tct ata ttt aaa tct tcg aga cca ata tat ctt gca agc   1026
Leu Leu Ile Ser Ile Phe Lys Ser Ser Arg Pro Ile Tyr Leu Ala Ser
              295                300                305
caa gag ggc cag ctg cct ttg cta ttt aat aca ctt aat agt cac tct   1074
Gln Glu Gly Gln Leu Pro Leu Leu Phe Asn Thr Leu Asn Ser His Ser
310                315                320                325
tct cca ttt aca gct gtg cta cta ctt gtc act ttg gga tcc ctt gca   1122
Ser Pro Phe Thr Ala Val Leu Leu Leu Val Thr Leu Gly Ser Leu Ala
                   330                335                340
att atc tta aca agt cta att gat ttg ata aac tat att ttt ttc acg   1170
Ile Ile Leu Thr Ser Leu Ile Asp Leu Ile Asn Tyr Ile Phe Phe Thr
              345                350                355
ggt tca tta tgg tct ata tta tta atg ata gga ata cta agg cgg aga   1218
Gly Ser Leu Trp Ser Ile Leu Leu Met Ile Gly Ile Leu Arg Arg Arg
              360                365                370
tac cag gaa ccc aat cta tct ata cct tat aag gta aaa ttg gat ttc   1266
Tyr Gln Glu Pro Asn Leu Ser Ile Pro Tyr Lys Val Lys Leu Asp Phe
              375                380                385
taat tcttttctgt gtgaaataac agatattgag tataactgta tttaagatta       1320
taatcagagc atctataagt agatcttctg aatactcagt tactgtgaaa cacatg      1376
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<210> 82

<211> 2392

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)...(1068)

<400> 82

gaagggtcgt tggtgggaaa g atg gcg gcg act ctg gga ccc ctt ggg tcg   51

                          Met Ala Ala Thr Leu Gly Pro Leu Gly Ser

                          1   5   10

tgg cag cag tgg cgg cga tgt ttg tcg gct cgg gat ggg tcc agg atg   99

Trp Gln Gln Trp Arg Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met

            15   20   25

tta ctc ctt ctt ctt ttg ttg ggg tct ggg cag ggg cca cag caa gtc   147

Leu Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val

        30   35   40

ggg gcg ggt caa acg ttc gag tac ttg aaa cgg gag cac tcg ctg tcg   195

Gly Ala Gly Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser

        45   50   55

aag ccc tac cag ggt gtg ggc aca ggc agt tcc tca ctg tgg aat ctg   243

Lys Pro Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu

        60   65   70

atg ggc aat gcc atg gtg atg acc cag tat atc cgc ctt acc cca gat   291

Met Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp

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        75                  80                  85                  90
atg caa agt aaa cag ggt gcc ttg tgg aac cgg gtg cca tgt ttc ctg    339
Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe Leu
                    95                  100                 105
aga gac tgg gag ttg cag gtg cac ttc aaa atc cat gga caa gga aag    387
Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly Lys
                    110                 115                 120
aag aat ctg cat ggg gat ggc ttg gca atc tgg tac aca aag gat cgg    435
Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg
                125                 130                 135
atg cag cca ggg cct gtg ttt gga aac atg gac aaa ttt gtg ggg ctg    483
Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly Leu
            140                 145                 150
gga gta ttt gta gac acc tac ccc aat gag gag aag cag caa gag cgg    531
Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg
155                 160                 165                 170
gta ttc ccc tac atc tca gcc atg gtg aac aac ggc tcc ctc agc tat    579
Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr
                    175                 180                 185
gat cat gag cgg gat ggg cgg cct aca gag ctg gga ggc tgc aca gcc    627
Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala
                    190                 195                 200
att gtc cgc aat ctt cat tac gac acc ttc ctg gtg att cgc tac gtc    675
Ile Val Arg Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val
                    205                 210                 215
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aag agg cat ttg acg ata atg atg gat att gat ggc aag cat gag tgg          723
Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp
    220             225             230

agg gac tgc att gaa gtg ccc gga gtc cgc ctg ccc cgc ggc tac tac          771
Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr
235             240             245             250

ttc ggc acc tcc tcc atc act ggg gat ctc tca gat aat cat gat gtc          819
Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val
                255             260             265

att tcc ttg aag ttg ttt gaa ctg aca gtg gag aga acc cca gaa gag          867
Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu
                270             275             280

gaa aag ctc cat cga gat gtg ttc ttg ccc tca gtg gac aat atg aag          915
Glu Lys Leu His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys
            285             290             295

ctg cct gag atg aca gct cca ctg ccg ccc ctg agt ggc ctg gcc ctc          963
Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu
    300             305             310

ttc ctc atc gtc ttt ttc tcc ctg gtg ttt tct gta ttt gcc ata gtc         1011
Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
315             320             325             330

att ggt atc ata ctc tac aac aaa tgg cag gaa cag agc cga aag cgc         1059
Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg
                335             340             345

ttc tac tgagc cctcctgctg ccaccacttt tgtgactgtc acccatgagg              1110
Phe Tyr
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Phe Tyr

tatggaagga gcaggcactg gcctgagcat gcagcctgga gagtgttctt gtctctagca   1170

gctggttggg gactatattc tgtcactgga gttttgaatg cagggacccc gcattcccat   1230

ggttgtgcat ggggacatct aactctggtc tgggaagcca cccaccccag ggcaatgctg   1290

ctgtgatgtg cctttccctg cagtccttcc atgtgggagc agaggtgtga agagaattta   1350

cgtggttgtg atgccaaaat cacagaacag aatttcatag cccaggctgc cgtgttgttt   1410

gactcagaag gcccttctac ttcagttttg aatccacaaa gaattaaaaa ctggtaacac   1470

cacaggcttt ctgaccatcc attcgttggg ttttgcattt gacccaaccc tctgcctacc   1530

tgaggagctt tctttggaaa ccaggatgga aacttcttcc ctgccttacc ttcctttcac   1590

tccattcatt gtcctctctg tgtgcaacct gagctgggaa aggcatttgg atgcctctct   1650

gttggggcct ggggctgcag aacacacctg cgtttcactg gccttcatta ggtggcccta   1710

gggagatggc tttctgcttt ggatcactgt tccctagcat gggtcttggg tctattggca   1770

tgtccatggc cttcccaatc aagtctcttc aggccctcag tgaagtttgg ctaaaggttg   1830

gtgtaaaaat caagagaagc ctggaagaca tcatggatgc catggattag ctgtgcaact   1890

gaccagctcc aggtttgatc aaaccaaaag caacatttgt catgtggtct gaccatgtgg   1950

agatgtttct ggacttgcta gagcctgctt agctgcatgt tttgtagtta cgatttttgg   2010

aatcccactt tgagtgctga aagtgtaagg aagctttctt cttacacctt gggcttggat   2070

attgcccaga gaagaaattt ggcttttttt ttcttaatgg acaagagaca gttgctgttc   2130

tcatgttcca agtctgagag caacagaccc tcatcatctg tgcctggaag agttcactgt   2190

cattgagcag cacagcctga gtgctggcct ctgtcaaccc ttattccact gccttatttg   2250

acaaggggtt acatgctgct caccttactg ccctgggatt aaatcagtta caggccagag   2310

tctccttgga gggcctggaa ctctgagtcc tcctatgaac ctctgtagcc taaatgaaat   2370

tcttaaaatc accgatggaa cc   2392

<210> 83

<211> 1416

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (55)...(840)

<400> 83

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                                                                   1

gaa ctg ctt caa gtg acc att ctt ttt ctt ctg ccc agt att tgc agc       105
Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser
            5                   10                  15

agt aac agc aca ggt gtt tta gag gca gct aat aat tca ctt gtt gtt       153
Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val
        20                  25                  30

act aca aca aaa cca tct ata aca aca cca aac aca gaa tca tta cag       201
Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu Gln
        35                  40                  45

aaa aat gtt gtc aca cca aca act gga aca act cct aaa gga aca atc       249
Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr Ile
50                  55                  60                  65

acc aat gaa tta ctt aaa atg tct ctg atg tca aca gct act ttt tta       297
Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe Leu
                70                  75                  80
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aca agt aaa gat gaa gga ttg aaa gcc aca acc act gat gtc agg aag        345
Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg Lys
            85                  90                  95

aat gac tcc atc att tca aac gta aca gta aca agt gtt aca ctt cca        393
Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu Pro
            100                 105                 110

aat gct gtt tca aca tta caa agt tcc aaa ccc aag act gaa act cag        441
Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr Gln
            115                 120                 125

agt tca att aaa aca aca gaa ata cca ggt agt gtt cta caa cca gat        489
Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro Asp
130                 135                 140                 145

gca tca cct tct aaa act ggt aca tta acc tca ata cca gtt aca att        537
Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr Ile
            150                 155                 160

cca gaa aac acc tca cag tct caa gta ata ggc act gag ggt gga aaa        585
Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Gly Thr Glu Gly Gly Lys
            165                 170                 175

aat gca agc act tca gca acc agc cgg tct tat tcc agt att att ttg        633
Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile Leu
            180                 185                 190

ccg gtg gtt att gct ttg att gta ata aca ctt tca gta ttt gtt ctg        681
Pro Val Val Ile Ala Leu Ile Val Ile Thr Leu Ser Val Phe Val Leu
            195                 200                 205

gtg ggt ttg tac cga atg tgc tgg aag gca gat ccg ggc aca cca gaa        729
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Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro Glu
210   215   220   225

aat gga aat gat caa cct cag tct gat aaa gag agc gtg aag ctt ctt   777
Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu Leu
                  230   235   240

acc gtt aag aca att tct cat gag tct ggt gag cac tct gca caa gga   825
Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln Gly
                  245   250   255

aaa acc aag aac tga cagcttgagg aattctctcc acacctaggc aataattacg   880
Lys Thr Lys Asn
            260

cttaatcttc agcttctatg caccaagcgt ggaaaaggag aaagtcctgc agaatcaatc   940
ccgacttcca tacctgctgc tggactgtac cagacgtctg tcccagtaaa gtgatgtcca   1000
gctgacatgc aataatttga tggaatcaaa aagaaccccg gggctctcct gttctctcac   1060
atttaaaaat tccattactc catttacagg agcgttccta ggaaaaggaa ttttaggagg   1120
agaatttgtg agcagtgaat ctgacagccc aggaggtggg ctcgctgata ggcatgactt   1180
tccttaatgt ttaaagtttt ccgggccaag aattttatc catgaagact ttcctacttt   1240
tctcggtgtt cttatattac ctactgttag tatttattgt ttaccactat gttaatgcag   1300
ggaaaagttg cacgtgtatt attaaatatt aggtagaaat cataccatgc tactttgtac   1360
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<210> 84

<211> 1347

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)...(694)

<400> 84

gccttgtgtt ttccaccctg aaaga atg ttg tgg ctg ctc ttt ttt ctg gtg   52

                         Met Leu Trp Leu Leu Phe Phe Leu Val

                         1   5

act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat gct ttt   100

Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala Phe

10   15   20   25

aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca tat gcc   148

Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala

                    30   35   40

tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct ttc tcc   196

Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser

                    45   50   55

atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat gtc cta   244

Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu

                    60   65   70

ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt aca gac   292

Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp

                    75   80   85

cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca gcc ata   340

Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile

90   95   100   105

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aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat gac caa        388
Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp Gln
            110             115             120

act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc atg gac        436
Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met Asp
            125             130             135

cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt tgc atc        484
Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys Ile
            140             145             150

atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg caa cgt        532
Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln Arg
        155             160             165

aga aga aag aac aaa gaa cca tct gaa gtg gat gac gct gaa gat aag        580
Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Asp Lys
170             175             180             185

tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat ccc ctg        628
Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro Leu
            190             195             200

gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag gat gag        676
Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp Glu
            205             210             215

agg ctc acc cct ctc tgaagggct gttgttctgc ttcctcaaga aattaaacat        730
Arg Leu Thr Pro Leu
            220

ttgtttctgt gtgactgctg agcatcctga aataccaaga gcagatcata tattttgttt     790
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caccattctt cttttgtaat aaattttgaa tgtgcttgaa agtgaaaagc aatcaattat      850

acccaccaac accactgaaa tcataagcta ttcacgactc aaaatattct aaaatatttt      910

tctgacagta tagtgtataa atgtggtcat gtggtatttg tagttattga tttaagcatt      970

tttagaaata agatcaggca tatgtatata ttttcacact tcaaagacct aaggaaaaat     1030

aaattttcca gtggagaata catataatat ggtgtagaaa tcattgaaaa tggatccttt     1090

ttgacgatca cttatatcac tctgtatatg actaagtaaa caaaagtgag aagtaattat     1150

tgtaaatgga tggataaaaa tggaattact catatacagg gtggaatttt atcctgttat     1210

cacaccaaca gttgattata tattttctga atatcagccc ctaataggac aattctattt     1270

gttgaccatt tctacaattt gtaaaagtcc aatctgtgct aacttaataa agtaataatc     1330

atctcttttt gattgtg                                                    1347
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<210> 85

<211> 2284

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)... (626)

<400> 85

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aggaattcag cccg atg gga gtc cga gtt cat gtc gtg gcg gcc tca gcc       110
              Met Gly Val Arg Val His Val Val Ala Ala Ser Ala
                1               5               10

ctg ctg tat ttc atc ctg ctt tct ggg acg aga tgt gag gaa aac tgt      158
Leu Leu Tyr Phe Ile Leu Leu Ser Gly Thr Arg Cys Glu Glu Asn Cys
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              15                  20                  25
ggt aat cct gaa cat tgc ctg acc aca gac tgg gta cat ctc tgg tat     206
Gly Asn Pro Glu His Cys Leu Thr Thr Asp Trp Val His Leu Trp Tyr

              30                  35                  40
ata tgg ttg cta gtg gta att ggc gcg ctg ctt ctc ctg tgt ggc ctg     254
Ile Trp Leu Leu Val Val Ile Gly Ala Leu Leu Leu Cys Gly Leu

           45                  50                  55              60
acg tcc ctg tgc ttc cgc tgc tgc tgt ctg agc cgc cag caa aat ggg     302
Thr Ser Leu Cys Phe Arg Cys Cys Cys Leu Ser Arg Gln Gln Asn Gly

                      65                  70                  75
gaa gat ggg ggc cca cca ccc tgt gaa gtg acc gtc att gct ttc gat     350
Glu Asp Gly Gly Pro Pro Pro Cys Glu Val Thr Val Ile Ala Phe Asp

                   80                  85                  90
cac gac agc act ctc cag agc act atc aca tct ctg cag tcg gtg ttt     398
His Asp Ser Thr Leu Gln Ser Thr Ile Thr Ser Leu Gln Ser Val Phe

                   95                 100                 105
ggc cct gca gct cgg agg atc ctg gct gtg gct cac tcc cac agc tcc     446
Gly Pro Ala Ala Arg Arg Ile Leu Ala Val Ala His Ser His Ser Ser

              110                 115                 120
ctg ggc cag ctg ccc tcc tct ttg gac acc ctc cca ggg tat gaa gaa     494
Leu Gly Gln Leu Pro Ser Ser Leu Asp Thr Leu Pro Gly Tyr Glu Glu

125                 130                 135                 140
gct ctt cac atg agt cgc ttc aca gta gcc atg tgc ggg cag aaa gca     542
Ala Leu His Met Ser Arg Phe Thr Val Ala Met Cys Gly Gln Lys Ala

                   145                 150                 155
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cct gat cta ccc cca gta cct gaa gaa aag cag ctg cct cca aca gag   590
Pro Asp Leu Pro Pro Val Pro Glu Glu Lys Gln Leu Pro Pro Thr Glu
            160   165   170

aag gag tcg act cga ata gtt gac tct tgg aac tgatgag agctgtcatt   640
Lys Glu Ser Thr Arg Ile Val Asp Ser Trp Asn

        175   180

ttataaatag gagtggagtg atgtccagag tctgtgggaa aatggaacac atacttttct   700

aaccctcaga agttttaaga tggcatctaa caccatcatt ctatgggaaa gatggttctt   760

actcttcgtt cacaggcctt tatatcttcc gatacagaat gctctaattg ggaactctaa   820

ttttgtatcc aatggccaaa atctgcaagt aatctctagc cacactgatt actactaaac   880

caggaaagca tcaaggtatc ttgaattcct ttaactattg agtgcatata gaattcctgt   940

acccacatga tactgcaagt tgtgtctctc tctgtcagct aatccactgc ggttaactgg   1000

aaaagaaaga caacagtgtc agcacagcca tcgacattaa tgcactgaat gcatgcatct   1060

ttcctcctga cacagcaatc gattttacac cgaatgacaa tgatcatctt agacagcaca   1120

acatacccac tcggatatct aaaagctagg gatggcattg ctgatatggg caaagagaac   1180

acagtatagt atttaagtgc caaatatcag tctttctttc tctctggtcc tacccctcag   1240

cagtatgaaa aactccatac tgtgcagtca cagttggatt aattcttcag ttcctccgca   1300

ctgcaaacac atatatgtgc gcacatgcat gtatacctgc accctgtttt aactctaaag   1360

gaatagtgtt gctttacttc tttcctgttt tgcctggacc acttaaagcc acaacacctc   1420

tatagtgaca cacgctagtc tctagtggtg gccctcactg ccacctagag gagccatggt   1480

ggaaaacaca ctctctcctt tgagcctatc tgcacatctc tcgagttctt ggagcaaaaa   1540

ctaaatgctg aactaagcct ggttgagatg cttcccatgg accatgccgc agcacagtgc   1600

taatctatcc acaaaacata ccacctccca aagtattatt attggaaaat cgaggaagtg   1660

acgcacattt agggaaaaac tactcacctt agagaagtca ctgaaatcct tttttttttt   1720

tttgagatgg agttttgctc ttgtagccca ggctgggatg caatggcatg gtctcagctc   1780

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actgtaacct ccacctcccg gattcaagca attcttctgc ctcagcttcc cgactagctg    1840

ggattacagc tgcctgccac cgtgcccagc taatttttgt attttttagtg gagaggggt    1900

ttcaccatgt tggccagtct ggtctagaac tcctgacgtc aggtgatccg cccaccttgg    1960

cctcccaaag tgctggaatt agaggcctga ccccctgctc ctggcctgaa atctttaaag    2020

ccgttttttc cctaaaaaac gggaaataat aacacctcag aaggtttttg tgaagatcaa    2080

agaagctaaa tatatgtggc atgatttgta aagtgttatg catatgtatg ttattcttcc    2140

tactgtcttc taaccttccc ttgcctgcta tgacttatct gagagccatg ttcccattta    2200

tcttttgcc aactatgtta ctgttgtcac acctgaaatg gctttgtttt tatcaataaa    2260

tacttgttga ttgtggtaaa cagc    2284
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<210> 86

<211> 1737

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (236)...(1024)

<400> 86

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gccggcccca ggcggtgctt ctccccacca ccgcccagct cagctcagcc cagcccagcc    120

cactctgccc ttagaggccc ttctccccaa agacgcactc cagaagtctc gccctcgtgc    180

ggctgaggag cctgggatcc cagacctgaa caagtgaaac ccccgcccct gaaga atg    238
                                                                   Met
                                                                     1

ggt aag acg ttt tcc cag ctg ggc tct tgg cgg gag gat gag aac aag    286
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Gly Lys Thr Phe Ser Gln Leu Gly Ser Trp Arg Glu Asp Glu Asn Lys

            5   10   15

tca atc ctg tcc tcc aaa cca gcc att ggc agc aag gct gtc aac tac   334

Ser Ile Leu Ser Ser Lys Pro Ala Ile Gly Ser Lys Ala Val Asn Tyr

            20   25   30

tcc agc acc ggt agc agc aag tct ttt tgt tcc tgt gtg cct tgt gaa   382

Ser Ser Thr Gly Ser Ser Lys Ser Phe Cys Ser Cys Val Pro Cys Glu

            35   40   45

gga act gct gat gcc agc ttc gtg act tgt ccc acc tgc cag ggc agt   430

Gly Thr Ala Asp Ala Ser Phe Val Thr Cys Pro Thr Cys Gln Gly Ser

50   55   60   65

ggc aag att ccc caa gag ctg gag aag cag ttg gtg gct ctc att ccc   478

Gly Lys Ile Pro Gln Glu Leu Glu Lys Gln Leu Val Ala Leu Ile Pro

            70   75   80

tat ggg gac cag agg ctg aag ccc aag cac acg aag ctc ttt gtg ttc   526

Tyr Gly Asp Gln Arg Leu Lys Pro Lys His Thr Lys Leu Phe Val Phe

            85   90   95

ctg gcc gtg ctc atc tgc ctg gtg acc tcc tcc ttc atc gtc ttt ttc   574

Leu Ala Val Leu Ile Cys Leu Val Thr Ser Ser Phe Ile Val Phe Phe

           100   105   110

ctg ttt ccc cgg tcc gtc att gtg cag cct gca ggc ctc aac tcc tcc   622

Leu Phe Pro Arg Ser Val Ile Val Gln Pro Ala Gly Leu Asn Ser Ser

           115   120   125

aca gtg gcc ttt gat gag gct gat atc tac ctc aac ata acg aat atc   670

Thr Val Ala Phe Asp Glu Ala Asp Ile Tyr Leu Asn Ile Thr Asn Ile

```
      130              135              140              145

tta aac atc tcc aat ggc aac tac tac ccc att atg gtg aca cag ctg      718
Leu Asn Ile Ser Asn Gly Asn Tyr Tyr Pro Ile Met Val Thr Gln Leu
                 150              155              160

acc ctc gag gtt ctg cac ctg tcc ctc gtg gtg ggg cag gtt tcc aac      766
Thr Leu Glu Val Leu His Leu Ser Leu Val Val Gly Gln Val Ser Asn
                 165              170              175

aac ctt ctc cta cac att ggc cct ttg gcc agt gaa cag atg ttt tac      814
Asn Leu Leu Leu His Ile Gly Pro Leu Ala Ser Glu Gln Met Phe Tyr
             180              185              190

gca gta gct acc aag ata cgg gat gaa aac aca tac aaa atc tgt acc      862
Ala Val Ala Thr Lys Ile Arg Asp Glu Asn Thr Tyr Lys Ile Cys Thr
         195              200              205

tgg ctg gaa atc aaa gtc cac cat gtg ctt ttg cac atc cag ggc acc      910
Trp Leu Glu Ile Lys Val His His Val Leu Leu His Ile Gln Gly Thr
210              215              220              225

ctg acc tgt tca tac ctg agc cat tca gag cag ctg gtc ttt cag agc      958
Leu Thr Cys Ser Tyr Leu Ser His Ser Glu Gln Leu Val Phe Gln Ser
                 230              235              240

tat gaa tat gtg gac tgc cga gga aac gca tct gtg ccc cac cag ctg      1006
Tyr Glu Tyr Val Asp Cys Arg Gly Asn Ala Ser Val Pro His Gln Leu
             245              250              255

acc cct cac cca cca tgacctgtc tgctgtccct gtactccagg cacctgcaac      1060
Thr Pro His Pro Pro
         260
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cctggtctat atctcccaca actccctggt gactaaggaa ggactacaga ggctttgcca   1120

aaggagaagc cctgcctcat cacacccta cctcccacccc cctcagcaca ggaagcttgc   1180

tttgaagtta acttcataca cacacactca tatcctccag tttcccccag attctttcag   1240

gggctgccat cagattctgc ccttggttag tttttgttt ttttttttgg tagagacaga   1300

gtctcactgt tggtccaggt tggttttgaa ctcctgggct caagcgatcc tcccttcttg   1360

gcctcccaaa gcacttggat tacagatgtg agcctgtgcc tggctggtct ttcttgagga   1420

aaatctgacc tggcattttc ttgaggcacc ttagattccc tggagtggca cctggccttt   1480

ctgtactgag cacctggtca gtctgaaggg ggcatttcac cccagctcca tcagggctgg   1540

cagtcccgtc tgaatgtgga gagagctgta gttttatctg gcttttaaaa catggacctg   1600

ccggctgggc gcagtggctt acacctgtaa tcccagtact ttgggaggcc gaagtgggtg   1660

gatcacttga gggcaggagt tcgtgaccag cctggtcaac atggtgaaac cttgtctcta   1720

ctaaaaatac aaaaatt   1737

<210> 87

<211> 1556

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)...(609)

<400> 87

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gctccccggc accagaagtt cctctgcgcg tccgacggcg ac atg ggc gtc ccc   114

                                                             Met Gly Val Pro

                                                                  1

```
acg gcc ctg gag gcc ggc agc tgg cgc tgg gga tcc ctg ctc ttc gct        162
Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser Leu Leu Phe Ala
 5                  10                15                20

ctc ttc ctg gct gcg tcc cta ggc aaa gat gca cca tcc aac tgt gtg        210
Leu Phe Leu Ala Ala Ser Leu Gly Lys Asp Ala Pro Ser Asn Cys Val
                25                30                35

gtg tac cca tcc tcc tcc cag gag agt gaa aac atc acg gct gca gcc        258
Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile Thr Ala Ala Ala
                40                45                50

ctg gct acg ggt gcc tgc atc gta gga atc ctc tgc ctc ccc ctc atc        306
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu Ile
                55                60                65

ctg ctc ctg gtc tac aag caa agg cag gca gcc tcc aac cgc cgt gcc        354
Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg Arg Ala
                70                75                80

cag gag ctg gtg cgg atg gac agc aac att caa ggg att gaa aac ccc        402
Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile Glu Asn Pro
85                  90                95                100

ggc ttt gaa gcc tca cca cct gcc cag ggg ata ccc gag gcc aaa gtc        450
Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu Ala Lys Val
                105                110                115

agg cac ccc ctg tcc tat gtg gcc cag cgg cag cct tct gag tct ggg        498
Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro Ser Glu Ser Gly
                120                125                130

cgg cat ctg ctt tcg gag ccc agc acc ccc ctg tct cct cca ggc ccc        546
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Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser Pro Pro Gly Pro

   135   140   145

gga gac gtc ttc ttc cca tcc ctg gac cct gtc cct gac tct cca aac   594

Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro Asp Ser Pro Asn

   150   155   160

ttt gag gtc atc tagc ccagctgggg gacagtgggc tgttgtggct gggtctgggg   650

Phe Glu Val Ile

165

caggtgcatt tgagccaggg ctggctctgt gagtggcctc cttggcctcg ccctggttc   710

cctccctcct gctctgggct cagatactgt gacatcccag aagcccagcc cctcaacccc   770

tctggatgct acatggggat gctggacggc tcagcccctg ttccaaggat tttggggtgc   830

tgagattctc ccctagagac ctgaaattca ccagctacag atgccaaatg acttacatct   890

taagaagtct cagaacgtcc agcccttcag cagctctcgt tctgagacat gagccttggg   950

atgtggcagc atcagtggga caagatggac actgggccac cctcccaggc accagacaca   1010

gggcacggtg gagagacttc tcccccgtgg ccgccttggc tcccccgttt tgcccgaggc   1070

tgctcttctg tcagacttcc tctttgtacc acagtggctc tggggccagg cctgcctgcc   1130

cactggccat cgccaccttc cccagctgcc tcctaccagc agtttctctg aagatctgtc   1190

aacaggttaa gtcaatctgg ggcttccact gcctgcattc cagtccccag agcttggtgg   1250

tcccgaaacg ggaagtacat attggggcat ggtggcctcc gtgagcaaat ggtgtcttgg   1310

gcaatctgag gccaggacag atgttgcccc acccactgga gatggtgctg agggaggtgg   1370

gtggggcctt ctgggaaggt gagtggagag gggcacctgc cccccgccct ccccatcccc   1430

tactcccact gctcagcgcg ggccattgca agggtgccac acaatgtctt gtccaccctg   1490

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ccctgg   1556

<210> 88

<211> 1855

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222)... (953)

<400> 88

cagagatgga atttcaccgt gttgcctagg ctggtctgga gctcttgatc tcaagcgatc　　60

ctccctgcct cggcctccca acgtgctggg attataggcg tgagccaccg ctcctggcca　　120

gggtctgttc ctagttgcaa cagttcttgg aaacccactc gagagggcca cgcctccatt　　180

caccaggcca cgcatcacaa gaggcaacac caggagccaa c atg agc tcg ggg　　233
　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　Met Ser Ser Gly
　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　1

act gaa ctg ctg tgg ccc gga gca gcg ctg ctg gtg ctg ttg ggg gtg　　281
Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val Leu Leu Gly Val
　5　　　　　　　　　10　　　　　　　　　15　　　　　　　　　20

gca gcc agt ctg tgt gtg cgc tgc tca cgc cca ggt gca aag agg tca　　329
Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro Gly Ala Lys Arg Ser
　　　　　　　　　25　　　　　　　　　30　　　　　　　　　35

gag aaa atc tac cag cag aga agt ctg cgt gag gac caa cag agc ttt　　377
Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp Gln Gln Ser Phe
　　　　　　　　　40　　　　　　　　　45　　　　　　　　　50

acg ggg tcc cgg acc tac tcc ttg gtc ggg cag gca tgg cca gga ccc　　425
Thr Gly Ser Arg Thr Tyr Ser Leu Val Gly Gln Ala Trp Pro Gly Pro

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                55                    60                    65

ctg gcg gac atg gca ccc aca agg aag gac aag ctg ttg caa ttc tac        473
Leu Ala Asp Met Ala Pro Thr Arg Lys Asp Lys Leu Leu Gln Phe Tyr
            70                    75                    80

ccc agc ctg gag gat cca gca tct tcc agg tac cag aac ttc agc aaa        521
Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr Gln Asn Phe Ser Lys
        85                    90                    95                    100

gga agc aga cac ggg tcg gag gaa gcc tac ata gac ccc att gcc atg        569
Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile Asp Pro Ile Ala Met
                    105                   110                   115

gag tat tac aac tgg ggg cgg ttc tcg aag ccc cca gaa gat gat gat        617
Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro Pro Glu Asp Asp Asp
                120                   125                   130

gcc aat tcc tac gag aat gtg ctc att tgc aag cag aaa acc aca gag        665
Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln Lys Thr Thr Glu
                135                   140                   145

aca ggt gcc cag cag gag ggc ata ggt ggc ctc tgc aga ggg gac ctc        713
Thr Gly Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys Arg Gly Asp Leu
                150                   155                   160

agc ctg tca ctg gcc ctg aag act ggc ccc act tct ggt ctc tgt ccc        761
Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser Gly Leu Cys Pro
165                   170                   175                   180

tct gcc tcc ccg gaa gaa gat gag gaa tct gag gat tat cag aac tca        809
Ser Ala Ser Pro Glu Glu Asp Glu Glu Ser Glu Asp Tyr Gln Asn Ser
                185                   190                   195
```

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gca tcc atc cat cag tgg cgc gag tcc agg aag gtc atg ggg caa ctc      857
Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val Met Gly Gln Leu
          200             205                 210

cag aga gaa gca tcc cct ggc ccg gtg gga agc cca gac gag gag gac      905
Gln Arg Glu Ala Ser Pro Gly Pro Val Gly Ser Pro Asp Glu Glu Asp
          215             220                 225

ggg gaa ccg gat tac gtg aat ggg gag gtg gca gcc aca gaa gcc          950
Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala Thr Glu Ala
          230             235                 240

tagggcagac caagaagaaa ggagccaagg caaagaggga ccactgtgct catggaccca   1010

tcgctgcctt ccaaggacca tttcccagag ctactcaact tttaagcccc tgccatggtt   1070

gctcctggaa ggagaaccag ccaccctgag gaccacctgg ccatgcgtgc acagcctggg   1130

aaaagacagt tactcacggg agctgcaggc ccgtcaccaa gccctctccc gacccaggct   1190

ttgtggggca ggcacctggt accaagggta acccggctcc tggtatggac ggatgcgcag   1250

gatttaggat aagctgtcac ccagtcccca taacaaaacc actgtccaac actggtatct   1310

gtgttctttt gtgctatgaa tttggattcc taattgctat tgttggttgc tggggtttta   1370

aatgattgat aagcttgtac agttaactta tagaggggga gccatattta acattctgga   1430

tttcagagta gagatttctg tgttgtctcc tagaaagcat tacatgtagt ttatttcagc   1490

atccttgttg ggtggggccc tggctctctt cccctttggt gggacctccc ctttctttgg   1550

gcttcagttc actcaggaag aaatgaggct gtcgccatct ttatgtgctt ccagtggaaa   1610

tgtcacttgc tacagacaat agtgcatgag agtctagaga agtagtgacc agaacagggc   1670

agagtaggtc ccctccatgg ccctgaatcc tcctctgctc cagggctggc ctctgcagag   1730

ctgattaaac agtgttgtga ctgtctcatg ggaagagctg gggcccagag ggaccttgag   1790

tcagaaatgt tgccagaaaa agtatctcct ccaaccaaaa catctcaata aaaccatttt   1850

agttg                                                               1855
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<210> 89

<211> 2530

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28)... (1314)

<400> 89

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                              Met Ala Arg Ser Leu Cys Pro Gly
                               1               5

gcc tgg cta agg aaa ccc tat tac ctc cag gct cgc ttc tca tat gtg          99
Ala Trp Leu Arg Lys Pro Tyr Tyr Leu Gln Ala Arg Phe Ser Tyr Val
        10              15              20

cgg atg aaa tat ctt ttc ttt tcc tgg tta gtg gtt ttt gtt gga agc         147
Arg Met Lys Tyr Leu Phe Phe Ser Trp Leu Val Val Phe Val Gly Ser
 25              30              35              40

tgg att ata tat gtg cag tat tct acc tat aca gaa tta tgc aga gga         195
Trp Ile Ile Tyr Val Gln Tyr Ser Thr Tyr Thr Glu Leu Cys Arg Gly
            45              50              55

aag gac tgt aag aaa ata ata tgt gac aag tac aag act gga gtt att         243
Lys Asp Cys Lys Lys Ile Ile Cys Asp Lys Tyr Lys Thr Gly Val Ile
            60              65              70

gat ggg cct gca tgt aac agc ctt tgt gtt aca gaa act ctt tac ttt         291
```

Asp Gly Pro Ala Cys Asn Ser Leu Cys Val Thr Glu Thr Leu Tyr Phe

     75   80   85

gga aaa tgt tta tcc acc aag ccc aac aat cag atg tat tta ggg att   339

Gly Lys Cys Leu Ser Thr Lys Pro Asn Asn Gln Met Tyr Leu Gly Ile

     90   95   100

tgg gat aat cta cca ggt gtt gtg aaa tgt caa atg gaa caa gcg ctt   387

Trp Asp Asn Leu Pro Gly Val Val Lys Cys Gln Met Glu Gln Ala Leu

105   110   115   120

cat ctt gat ttt gga act gaa ttg gaa cca aga aaa gaa ata gtg cta   435

His Leu Asp Phe Gly Thr Glu Leu Glu Pro Arg Lys Glu Ile Val Leu

         125   130   135

ttt gat aag cca act aga gga act act gta caa aaa ttt aaa gaa atg   483

Phe Asp Lys Pro Thr Arg Gly Thr Thr Val Gln Lys Phe Lys Glu Met

         140   145   150

gtc tat agt ctc ttt aag gca aaa ttg ggt gac caa gga aac ctc tct   531

Val Tyr Ser Leu Phe Lys Ala Lys Leu Gly Asp Gln Gly Asn Leu Ser

         155   160   165

gaa ctg gtt aat ctc atc ttg acg gtg gct gat gga gac aaa gat ggc   579

Glu Leu Val Asn Leu Ile Leu Thr Val Ala Asp Gly Asp Lys Asp Gly

170   175   180

cag gtt tcc ttg gga gaa gca aag tcg gca tgg gca ctt ctt caa ctg   627

Gln Val Ser Leu Gly Glu Ala Lys Ser Ala Trp Ala Leu Leu Gln Leu

185   190   195   200

aat gaa ttt ctt ctc atg gtg ata ctt caa gat aaa gaa cat acc ccc   675

Asn Glu Phe Leu Leu Met Val Ile Leu Gln Asp Lys Glu His Thr Pro

```
                  205                 210                 215
aaa tta atg gga ttc tgt ggt gac ctc tat gtg atg gaa agt gtt gaa        723
Lys Leu Met Gly Phe Cys Gly Asp Leu Tyr Val Met Glu Ser Val Glu

                  220                 225                 230
tat acc tct ctt tat gga ata agc ctt cct tgg gtc att gaa ctt ttt       771
Tyr Thr Ser Leu Tyr Gly Ile Ser Leu Pro Trp Val Ile Glu Leu Phe

                  235                 240                 245
att cca tct ggg ttc aga aga agc atg gat cag ctg ttc aca cca tca       819
Ile Pro Ser Gly Phe Arg Arg Ser Met Asp Gln Leu Phe Thr Pro Ser

                  250                 255                 260
tgg cca aga aag gcc aaa ata gcc ata gga ctt cta gaa ttt gtg gaa       867
Trp Pro Arg Lys Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val Glu
265                 270                 275                 280
gat gtt ttc cat ggc ccc tac gga aat ttc ctc atg tgc gat act agt       915
Asp Val Phe His Gly Pro Tyr Gly Asn Phe Leu Met Cys Asp Thr Ser

                  285                 290                 295
gcc aaa aac cta gga tat aat gat aag tat gat ttg aaa atg gtg gat       963
Ala Lys Asn Leu Gly Tyr Asn Asp Lys Tyr Asp Leu Lys Met Val Asp

                  300                 305                 310
atg aga aaa att gtg cca gag aca aac ctg aaa gaa ctt att aag gat      1011
Met Arg Lys Ile Val Pro Glu Thr Asn Leu Lys Glu Leu Ile Lys Asp

                  315                 320                 325
cgt cac tgt gag tct gat ttg gac tgt gtc tat ggc aca gat tgt aga      1059
Arg His Cys Glu Ser Asp Leu Asp Cys Val Tyr Gly Thr Asp Cys Arg

                  330                 335                 340
```

act agc tgt gat cag agt aca atg aag tgt act tca gaa gtg ata caa   1107
Thr Ser Cys Asp Gln Ser Thr Met Lys Cys Thr Ser Glu Val Ile Gln
345   350   355   360

cca aac ttg gca aaa gct tgt cag tta ctc aaa gac tac cta ctg cgt   1155
Pro Asn Leu Ala Lys Ala Cys Gln Leu Leu Lys Asp Tyr Leu Leu Arg
                365   370   375

ggt gct cca agt gaa att cgt gaa gaa tta gaa aag cag ctt tat tct   1203
Gly Ala Pro Ser Glu Ile Arg Glu Glu Leu Glu Lys Gln Leu Tyr Ser
                380   385   390

tgt att gct ctc aaa gtc aca gca aat caa atg gaa atg gaa cat tct   1251
Cys Ile Ala Leu Lys Val Thr Ala Asn Gln Met Glu Met Glu His Ser
        395   400   405

ttg ata cta aat aac cta aaa aca tta ttg tgg aag aaa att tcc tac   1299
Leu Ile Leu Asn Asn Leu Lys Thr Leu Leu Trp Lys Lys Ile Ser Tyr
        410   415   420

act aat gac tct tagttcatt tggacataat taccatttta agaaacctgc   1350
Thr Asn Asp Ser
425

cacttttaaa gaacaatttt gagcattaaa aaaaaatggc ttcaaattcc tgccagttac   1410

acaaaactcc ttccccccag gcctgagaag ccatcagtat gtgattactg aagtaatggc   1470

aggtgtagga tcaacaggtc cccaagatgt cattcctgcc cttttagaag ccctgttaca   1530

tctccgaagt acattcattg tgtaactatt ttgactgact ttaaaaacca atgctgtgaa   1590

aagcttcatt ccataaacat caacagtgag tgatttgtag atttacctta gccaaaatac   1650

caatgctgga agcattgtgt ttgcattgaa gctgctgttc aacaagaaaa tttataaatt   1710

tactaatgtc ttagcatggt aaagtttgca cattaacaga aattaagact gcaaagcagg   1770

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ttaaacttgc ttctttataa aacagatgtt gggttaatag catggtttac tgtattaaag    1830

acttatacac ccatttttaa cctcattcag acatcaagtt atgtgtagct tcacaatggt    1890

tcaagtggct tacttcaaga aatcttatac ttgacagtac accaatttta ttgactaaaa    1950

atggatgaac tttcctaaag attcaaaggg cccatcttag tatcacgcag ctgactgagc    2010

ccttcaaaac tgacatctta aggcccaatc aagatccaca tatcctgatt ttgaactatg    2070

tgaaagtggg actgttaagt gcaagactaa aataaattat agcagacttt ttagtaataa    2130

ctttccattt tcaaacagta tatcctgtgg gccaaagggc tatttcttaa agaggcatgt    2190

aaatgtattt atttatctaa tgttttttc cccatgtaaa cttgatatac aaggtttagt     2250

atttgctcct ctttcatatt attttcacac gtatactcag atttggcatg tacctttcaa    2310

catctccata aaattaaaca ccttttggag aaaagatcca ctattttctg ctcaaaggtt    2370

tcgcctacct aaagtggaac atgttaaaaa tctatgtgac catcactgga cagctttctc    2430

tcaaaacttt ccttcaacgc catggattag caccagtttt gtttacttta aggtactttt    2490

cccattcatc atctggttat aataaatgga tggaagaaat                          2530
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<210> 90

<211> 1911

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)... (1083)

<400> 90

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ttcagagctg tgactgcggc tgcactcaga gaagctgccc ttggctgctc gtagcgccgg     180
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```
gccttctctc ctcgtcatca tccagagcag ccagtgtccg ggaggcagaa g atg ccc       237
                                                           Met Pro
                                                             1

cac tcc agc ctg cat cca tcc atc ccg tgt ccc agg ggt cac ggg gcc       285
His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala
          5                   10                  15

cag aag gca gcc ttg gtt ctg ctg agt gcc tgc ctg gtg acc ctt tgg       333
Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp
       20                  25                  30

ggg cta gga gag cca cca gag cac act ctc cgg tac ctg gtg ctc cac       381
Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His
    35                  40                  45                  50

cta gcc tcc ctg cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg       429
Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu
              55                  60                  65

gct gag gag ctg cac cac atc cac tcc agg tac cgg ggc agc tac tgg       477
Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp
           70                  75                  80

agg act gtg cgg gcc tgc ctg ggc tgc ccc ctc cgc cgt ggg gcc ctg       525
Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu
       85                  90                  95

ttg ctg ctg tcc atc tat ttc tac tac tcc ctc cca aat gcg gtc ggc       573
Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly
    100                 105                 110

ccg ccc ttc act tgg atg ctt gcc ctc ctg ggc ctc tcg cag gca ctg       621
```

Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu
115   120   125   130

aac atc ctc ctg ggc ctc aag ggc ctg gcc cca gct gag atc tct gca   669
Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala
                  135   140   145

gtg tgt gaa aaa ggg aat ttc aac gtg gcc cat ggg ctg gca tgg tca   717
Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser
                  150   155   160

tat tac atc gga tat ctg cgg ctg atc ctg cca gag ctc cag gcc cgg   765
Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg
                  165   170   175

att cga act tac aat cag cat tac aac aac ctg cta cgg ggt gca gtg   813
Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val
                  180   185   190

agc cag cgg ctg tat att ctc ctc cca ttg gac tgt ggg gtg cct gat   861
Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp
195   200   205   210

aac ctg agt atg gct gac ccc aac att cgc ttc ctg gat aaa ctg ccc   909
Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro
                  215   220   225

cag cag acc gct gac cgt gct ggc atc aag gat cgg gtt tac agc aac   957
Gln Gln Thr Ala Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn
                  230   235   240

agc atc tat gag ctt ctg gag aac ggg cag cgg aac ctg cag atg aca   1005
Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Asn Leu Gln Met Thr

```
        245                 250                 255
gca gct tct cgc tgt ccc agg agg ttc tcc ggc acc tgc ggc agg agg     1053
Ala Ala Ser Arg Cys Pro Arg Arg Phe Ser Gly Thr Cys Gly Arg Arg

        260                 265                 270
aaa agg aag agg tta ctg tgg gca gct tgaagacctc agcggtgccc          1100
Lys Arg Lys Arg Leu Leu Trp Ala Ala

275                 280
agtacctcca cgatgtccca agagcctgag ctcctcatca gtggaatgga aaagcccctc   1160

cctctccgca cggatttctc ttgagaccca gggtcaccag gccagagcct ccagtggtct   1220

ccaagcctct ggactggggg ctctcttcag tggctgaatg tccagcagag ctatttcctt   1280

ccacagggg ccttgcaggg aagggtccag gacttgacat cttaagatgc gtcttgtccc    1340

cttgggccag tcatttcccc tctctgagcc tcggtgtctt caacctgtga atgggatca    1400

taatcactgc cttacctccc tcacggttgt tgtgaggact gagtgtgtgg aagtttttca   1460

taaactttgg atgctagtgt acttaggggg tgtgccaggt gtctttcatg gggccttcca   1520

gacccactcc ccaccccttct ccccttcctt tgcccgggga cgccgaactc tctcaatggt   1580

atcaacaggc tccttcgccc tctggctcct ggtcatgttc cattattggg gagccccagc    1640

agaagaatgg agaggaggag gaggctgagt ttggggtatt gaatcccccg gctcccaccc    1700

tgcagcatca aggttgctat ggactctcct gccgggcaac tcttgcgtaa tcatgactat    1760

ctctaggatt ctggcaccac ttccttccct ggcccccttaa gcctagctgt gtatcggcac    1820

ccccacccca ctagagtact ccctctcact tgcggtttcc ttatactcca ccccttctc     1880

aacggtcctt ttttaaagca catctcagat t                                  1911
```

<210> 91

<211> 476

<212> PRT

<213> Homo sapiens

<400> 91

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
1   5   10   15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
                20   25   30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
        35   40   45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
    50   55   60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val
65   70   75   80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
                85   90   95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro
                100   105   110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
            115   120   125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
    130   135   140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
145   150   155   160

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
                165   170   175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu

```
              180               185               190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
          195               200               205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
      210               215               220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
225               230               235               240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
              245               250               255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
              260               265               270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu
          275               280               285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
      290               295               300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
305               310               315               320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
              325               330               335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
          340               345               350
Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
          355               360               365
Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
      370               375               380
```

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu His Ser Leu
385   390   395   400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
                 405   410   415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
                 420   425   430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
                 435   440   445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
            450   455   460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
465   470   475

<210> 92

<211> 226

<212> PRT

<213> Homo sapiens

<400> 92

Met Ser Arg Ala Gln Ile Trp Ala Leu Val Ser Gly Val Gly Gly Phe
1   5   10   15

Gly Ala Leu Val Ala Ala Thr Thr Ser Asn Glu Trp Lys Val Thr Thr
            20   25   30

Arg Ala Ser Ser Val Ile Thr Ala Thr Trp Val Tyr Gln Gly Leu Trp
            35   40   45

Met Asn Cys Ala Gly Asn Ala Leu Gly Ser Phe His Cys Arg Pro His

```
           50                  55                  60
Phe Thr Ile Phe Lys Val Ala Gly Tyr Ile Gln Ala Cys Arg Gly Leu

  65                  70                  75                  80
Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile Phe Ala Leu

                   85                  90                  95
Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys Ala Lys Ala

                  100                 105                 110
Lys Ile Ala Cys Leu Ala Gly Ile Val Phe Ile Leu Ser Gly Leu Cys

                  115                 120                 125
Ser Met Thr Gly Cys Ser Leu Tyr Ala Asn Lys Ile Thr Thr Glu Phe

                  130                 135                 140
Phe Asp Pro Leu Phe Val Glu Gln Lys Tyr Glu Leu Gly Ala Ala Leu

 145                 150                 155                 160
Phe Ile Gly Trp Ala Gly Ala Ser Leu Cys Ile Ile Gly Gly Val Ile

                  165                 170                 175
Phe Cys Phe Ser Ile Ser Asp Asn Asn Lys Thr Pro Arg Tyr Thr Tyr

                  180                 185                 190
Asn Gly Ala Thr Ser Val Met Ser Ser Arg Thr Lys Tyr His Gly Gly

                  195                 200                 205
Glu Asp Phe Lys Thr Thr Asn Pro Ser Lys Gln Phe Asp Lys Asn Ala

                  210                 215                 220
Tyr Val

 225
```

<210> 93

<211> 305

<212> PRT

<213> Homo sapiens

<400> 93

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
1   5   10   15

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
            20   25   30

Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
            35   40   45

Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
        50   55   60

Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
65   70   75   80

Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
                85   90   95

Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
                100   105   110

Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
            115   120   125

Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val
            130   135   140

Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
145   150   155   160

Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala

```
                    165                 170                 175
Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu
                    180                 185                 190
Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys
                    195                 200                 205
Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu
                    210                 215                 220
Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp
225                 230                 235                 240
Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe
                    245                 250                 255
Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp
                    260                 265                 270
Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys
                    275                 280                 285
His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr
                    290                 295                 300
Tyr

305
```

<210> 94

<211> 227

<212> PRT

<213> Homo sapiens

<400> 94

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
  1   5   10   15

Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
                20   25   30

Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
                35   40   45

Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
        50   55   60

Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
 65   70   75   80

Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
                85   90   95

Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
                100   105   110

Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
        115   120   125

Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
        130   135   140

Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
145   150   155   160

Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
                165   170   175

Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
                180   185   190

Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala

```
           195                 200                 205
Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile

           210                 215                 220
Ala Ala Cys

225
```

<210> 95

<211> 441

<212> PRT

<213> Homo sapiens

<400> 95

```
Met Ala Ile His Lys Ala Leu Val Met Cys Leu Gly Leu Pro Leu Phe
 1               5                  10                  15
Leu Phe Pro Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser
                20                  25                  30
Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala
                35                  40                  45
Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr
         50                  55                  60
Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp
 65                 70                  75                  80
Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly
                85                  90                  95
Thr Leu Gly Leu Phe Cys Leu Val Phe Ala Cys Val Val Lys Pro Asp
            100                 105                 110
```

Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu Phe Gly Val Leu Phe Ala
            115   120   125

Ile Cys Phe Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu
            130   135   140

Ala Arg Lys Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala
145   150   155   160

Leu Leu Leu Thr Leu Val Glu Val Ile Ile Asn Thr Glu Trp Leu Ile
                165   170   175

Ile Thr Leu Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser
                180   185   190

Ser Ala Gly Trp Ala Val Ala Ser Pro Cys Ala Ile Ala Asn Met Asp
                195   200   205

Phe Val Met Ala Leu Ile Tyr Val Met Leu Leu Leu Leu Gly Ala Phe
            210   215   220

Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg Tyr Lys Arg Trp Arg Lys
225   230   235   240

His Gly Val Phe Val Leu Leu Thr Thr Ala Thr Ser Val Ala Ile Trp
                245   250   255

Val Val Trp Ile Val Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser
                260   265   270

Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala
            275   280   285

Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr
            290   295   300

Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg

```
       305                    310                    315                    320
Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu Gln Lys Gly Gln Ser Met

                    325                    330                    335
Phe Val Glu Asn Lys Ala Phe Ser Met Asp Glu Pro Val Ala Ala Lys

               340                    345                    350
Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn Gly Gln Leu Leu Thr Ser

               355                    360                    365
Val Tyr Gln Pro Thr Glu Met Ala Leu Met His Lys Val Pro Ser Glu

          370                    375                    380
Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala Thr Ala Asn Ser Gln Val

385                    390                    395                    400
Met Gly Ser Ala Asn Ser Thr Leu Arg Ala Glu Asp Met Tyr Ser Ala

                    405                    410                    415
Gln Ser His Gln Ala Ala Thr Pro Pro Lys Asp Gly Lys Asn Ser Gln

               420                    425                    430
Val Phe Arg Asn Pro Tyr Val Trp Asp

     435                    440
```

<210> 96

<211> 265

<212> PRT

<213> Homo sapiens

<400> 96

```
Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
1               5                   10                  15
```

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
            20   25   30

Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val
            35   40   45

Ser Arg Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser
            50   55   60

Thr Pro Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser
65   70   75   80

Ile Ser Gln Ile Ser Thr Thr Leu Pro Pro Thr Thr Ser Thr Lys Lys
                    85   90   95

Ser Gly Gly Ala Ser Val Val Pro His Pro Ser Pro Thr Pro Leu Ser
                    100   105   110

Gln Glu Glu Ala Asp Asn Asn Glu Asp Pro Ser Ile Glu Glu Glu Asp
            115   120   125

Leu Leu Met Leu Asn Ser Ser Pro Ser Thr Ala Lys Asp Thr Leu Asp
            130   135   140

Asn Gly Asp Tyr Gly Glu Pro Asp Tyr Asp Trp Thr Thr Gly Pro Arg
145   150   155   160

Asp Asp Asp Glu Ser Asp Asp Thr Leu Glu Glu Asn Arg Gly Tyr Met
                    165   170   175

Glu Ile Glu Gln Ser Val Lys Ser Phe Lys Met Pro Ser Ser Asn Ile
                    180   185   190

Glu Glu Glu Asp Ser His Phe Phe Phe His Leu Ile Ile Phe Ala Phe
            195   200   205

Cys Ile Ala Val Val Tyr Ile Thr Tyr His Asn Lys Arg Lys Ile Phe

```
          210                    215                    220
Leu Leu Val Gln Ser Arg Lys Trp Arg Asp Gly Leu Cys Ser Lys Thr
225                    230                    235                    240
Val Glu Tyr His Arg Leu Asp Gln Asn Val Asn Glu Ala Met Pro Ser
                    245                    250                    255
Leu Lys Ile Thr Asn Asp Tyr Ile Phe
                    260                    265
```

<210> 97

<211> 208

<212> PRT

<213> Homo sapiens

<400> 97

```
Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala Val Phe
 1                   5                    10                   15
Ala Leu Leu Asp Val Trp Tyr Leu Val Arg Leu Pro Cys Ala Val Leu
                    20                   25                   30
Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala Glu Gln
          35                   40                   45
Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu Leu His
          50                   55                   60
Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg Val Ala
65                   70                   75                   80
His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu Leu Arg Ala
                    85                   90                   95
```

His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg Ser Leu Arg
           100   105   110

Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp Asp Asp
           115   120   125

Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp Gly Phe
           130   135   140

Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr Ser Pro
145   150   155   160

Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro Pro Glu
                167   170   175

Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala Ser Ser
                180   185   190

Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys Asp Gln
           195   200   205

<210> 98

<211> 400

<212> PRT

<213> Homo sapiens

<400> 98

Met Ala Trp Arg Arg Arg Glu Ala Ser Val Gly Ala Arg Gly Val Leu
1   5   10   15

Ala Leu Ala Leu Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly
           20   25   30

Arg Ala Leu Glu Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp

```
                35                      40                      45
Pro Gln Thr Asn Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe
                50                      55                      60
Gly Asp Ser Ser Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro
        65                      70                      75                      80
Trp Ala Pro Gly Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe
                        85                      90                      95
Phe Val Pro Glu Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu
                        100                     105                     110
Val Ala Arg Gly Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala
                115                     120                     125
Arg Arg Asn Ala Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly
                130                     135                     140
Asn Ile Thr Leu Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val
        145                     150                     155                     160
Ile Met Ile Ser Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln
                        165                     170                     175
Lys Gly Ile Pro Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val
                        180                     185                     190
Gln Glu Phe Ile Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe
                195                     200                     205
Ile Thr Met Met Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile
                210                     215                     220
Gln Arg Phe Leu Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg
225                     230                     235                     240
```

Lys Glu Thr Lys Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys
                245   250   255

His Gly Glu Lys Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys
                260   265   270

Ile Glu Asn Phe Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys
                275   280   285

His Ile Phe His Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg
        290   295   300

Thr Cys Pro Met Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp
305   310   315   320

Gly Glu Pro Gly Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro
                325   330   335

Gly Arg Asp Pro Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp
                340   345   350

Gly Ser Asp Glu Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu
                355   360   365

Pro Gln Cys Asp Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala
        370   375   380

Leu Leu Glu Ala Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser
385   390   395   400

<210> 99

<211> 192

<212> PRT

<213> Homo sapiens

<400> 99

Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp Tyr
1   5   10   15

Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr Val
            20   25   30

His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr Glu
            35   40   45

Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu His
        50   55   60

Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val Pro
65   70   75   80

Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu Cys
                85   90   95

Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln Gly
                100   105   110

Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe Lys
            115   120   125

Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Glu Leu Met
        130   135   140

Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val Phe Gln Ser Thr
145   150   155   160

Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe Ser Gly Arg Arg
                165   170   175

Ala Lys Val Thr Arg Arg Lys His His Cys Val Arg Glu Gly Ser Gly
                180   185   190

<210> 100

<211> 260

<212> PRT

<213> Homo sapiens

<400> 100

Met Ala Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala Gly Gly Val Gly
1   5   10   15

Leu Leu Val Leu Leu Leu Leu Gly Leu Phe Arg Pro Pro Pro Ala Leu
                20   25   30

Cys Ala Arg Pro Val Lys Glu Pro Arg Gly Leu Ser Ala Ala Ser Pro
                35   40   45

Pro Leu Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg Arg Ser Val Pro
      50   55   60

Arg Gly Glu Ala Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala
65   70   75   80

His Leu Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln
                85   90   95

Glu Ala Glu Asp Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Val
                100   105   110

Trp Gly Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly Leu Asp Asp Asp
      115   120   125

Pro Asp Ala Pro Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg
130   135   140

Leu Asp Pro Ala Ala Leu Ala Ala Gln Leu Val Pro Ala Pro Val Pro

```
            145                 150                 155                 160
Ala Ala Ala Leu Arg Pro Arg Pro Pro Val Tyr Asp Asp Gly Pro Ala
                    165                 170                 175
Gly Pro Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro Asp Val Asp Pro
                    180                 185                 190
Glu Leu Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala Gly Ser Ala Asp
                    195                 200                 205
Ser Glu Gly Val Ala Ala Pro Arg Arg Leu Arg Arg Ala Ala Asp His
                    210                 215                 220
Asp Val Gly Ser Glu Leu Pro Pro Glu Gly Val Leu Gly Ala Leu Leu
            225                 230                 235                 240
Arg Val Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg
                    245                 250                 255
Leu Leu Pro Pro
            260
```

<210> 101

<211> 1428

<212> DNA

<213> Homo sapiens

<400> 101

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atggttggtg ccatgtggaa ggtgattgtt tcgctggtcc tgttgatgcc tggcccctgt    60

gatgggctgt ttcgctccct atacagaagt gtttccatgc cacctaaggg agactcagga   120

cagccattat ttctcacccc ttacattgaa gctgggaaga tccaaaaagg aagagaattg   180

agtttggtcg gccctttccc aggactgaac atgaagagtt atgccggctt cctcaccgtg   240
```

```
aataagactt acaacagcaa cctcttcttc tggttcttcc cagctcagat acagccagaa    300

gatgccccag tagttctctg gctacagggt gggccgggag gttcatccat gtttggactc    360

tttgtggaac atgggcctta tgttgtcaca agtaacatga ccttgcgtga cagagacttc    420

ccctggacca caacgctctc catgctttac attgacaatc cagtgggcac aggcttcagt    480

tttactgatg atacccacgg atatgcagtc aatgaggacg atgtagcacg ggatttatac    540

agtgcactaa ttcagttttt ccagatattt cctgaatata aaaataatga cttttatgtc    600

actggggagt cttatgcagg gaaatatgtg ccagccattg cacacctcat ccattccctc    660

aaccctgtga gagaggtgaa gatcaacctg aacggaattg ctattggaga tggatattct    720

gatcccgaat caattatagg gggctatgca gaattcctgt accaaattgg cttgttggat    780

gagaagcaaa aaaagtactt ccagaagcag tgccatgaat gcatagaaca catcaggaag    840

cagaactggt ttgaggcctt tgaaatactg gataaactac tagatggcga cttaacaagt    900

gatccttctt acttccagaa tgttacagga tgtagtaatt actataactt tttgcggtgc    960

acggaacctg aggatcagct ttactatgtg aaattttgt cactcccaga ggtgagacaa   1020

gccatccacg tggggaatca gacttttaat gatggaacta tagttgaaaa gtacttgcga   1080

gaagatacag tacagtcagt taagccatgg ttaactgaaa tcatgaataa ttataaggtt   1140

ctgatctaca atggccaact ggacatcatc gtggcagctg ccctgacaga gcactccttg   1200

atgggcatgg actggaaagg atcccaggaa tacaagaagg cagaaaaaaa agtttggaag   1260

atctttaaat ctgacagtga agtggctggt tacatccggc aagcgggtga cttccatcag   1320

gtaattattc gaggtggagg acatattta ccctatgacc agcctctgag agcttttgac   1380

atgattaatc gattcattta tggaaaagga tgggatcctt atgttgga              1428
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<210> 102

<211> 678

<212> DNA

<213> Homo sapiens

<400> 102

atgtccaggg cgcagatctg ggctctggtg tctggtgtcg gagggtttgg agctctcgtt   60

gctgctacca cgtccaatga gtggaaagtg accacgcgag cctcctcggt gataacagcc   120

acttgggttt accagggtct gtggatgaac tgcgcaggta acgcgttggg ttctttccat   180

tgccgaccgc attttactat cttcaaagta gcaggttata tacaggcatg tagaggactt   240

atgatcgctg ctgtcagcct gggcttcttt ggttccatat ttgcgctctt tggaatgaag   300

tgtaccaaag tcggaggctc cgataaagcc aaagctaaaa ttgcttgttt ggctgggatt   360

gtattcatac tgtcagggct gtgctcaatg actggatgtt ccctatatgc aaacaaaatc   420

acaacggaat tctttgatcc tctctttgtt gagcaaaagt atgaattagg agccgctctg   480

tttattggat gggcaggagc ctcactgtgc ataattggtg gtgtcatatt ttgcttttca   540

atatctgaca acaacaaaac acccagatac acatacaacg gggccacatc tgtcatgtct   600

tctcggacaa agtatcatgg tggagaagat tttaaaacaa caaacccttc aaaacagttt   660

gataaaaatg cttatgtc   678

<210> 103

<211> 915

<212> DNA

<213> Homo sapiens

<400> 103

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ctggacccca atgaaaagta cctgctacga ctgctagaca agacgactgt gagccacaac   180

accaagaggt tccgctttgc cctgcccacc gcccaccaca ctctggggct gcctgtgggc   240

aaacatatct acctctccac ccgaattgat ggcagcctgg tcatcaggcc atacactcct   300

gtcaccagtg atgaggatca aggctatgtg gátcttgtca tcaaggtcta cctgaagggt   360

```
gtgcacccca aatttcctga gggagggaag atgtctcagt acctggatag cctgaaggtt   420

ggggatgtgg tggagtttcg ggggccaagc gggttgctca cttacactgg aaaagggcat   480

tttaacattc agcccaacaa gaaatctcca ccagaacccc gagtggcgaa gaaactggga   540

atgattgccg gcgggacagg aatcacccca atgctacagc tgatccgggc catcctgaaa   600

gtccctgaag atccaaccca gtgctttctg ctttttgcca accagacaga aaaggatatc   660

atcttgcggg aggacttaga ggaactgcag gcccgctatc ccaatcgctt taagctctgg   720

ttcactctgg atcatccccc aaaagattgg gcctacagca agggctttgt gactgccgac   780

atgatccggg aacacctgcc cgctccaggg gatgatgtgc tggtactgct ttgtgggcca   840

ccccaatgg tgcagctggc ctgccatccc aacttggaca aactgggcta ctcacaaaag   900

atgcgattca cctac                                                   915
```

<210> 104

<211> 681

<212> DNA

<213> Homo sapiens

<400> 104

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atgggttgga caatgaggct ggtcacagca gcactgttac tgggtctcat gatggtggtc    60

actggagacg aggatgagaa cagcccgtgt gcccatgagg ccctcttgga cgaggacacc   120

ctcttttgcc agggccttga agttttctac ccagagttgg ggaacattgg ctgcaaggtt   180

gttcctgatt gtaacaacta cagacagaag atcacctcct ggatggagcc gatagtcaag   240

ttcccggggg ccgtggacgg cgcaacctat atcctggtga tggtggatcc agatgcccct   300

agcagagcag aacccagaca gagattctgg agacattggc tggtaacaga tatcaagggc   360

gccgacctga agaaagggaa gattcagggc caggagttat cagcctacca ggctccctcc   420

ccaccggcac acagtggctt ccatcgctac cagttctttg tctatcttca ggaaggaaaa   480

gtcatctctc tccttcccaa ggaaaacaaa actcgaggct cttggaaaat ggacagattt   540
```

ctgaaccgtt tccacctggg cgaacctgaa gcaagcaccc agttcatgac ccagaactac   600

caggactcac caaccctcca ggctcccaga gaaagggcca gcgagcccaa gcacaaaaac   660

caggcggaga tagctgcctg c   681

<210> 105

<211> 1323

<212> DNA

<213> Homo sapiens

<400> 105

atggccatcc acaaagcctt ggtgatgtgc ctgggactgc ctctcttcct gttcccaggg   60

gcctgggccc agggccatgt cccacccggc tgcagccaag gcctcaaccc cctgtactac   120

aacctgtgtg accgctctgg ggcgtggggc atcgtcctgg aggccgtggc tggggcgggc   180

attgtcacca cgtttgtgct caccatcatc ctggtggcca gcctcccctt tgtgcaggac   240

accaagaaac ggagcctgct ggggacccag gtattcttcc ttctggggac cctgggcctc   300

ttctgcctcg tgtttgcctg tgtggtgaag cccgacttct ccacctgtgc ctctcggcgc   360

ttcctctttg gggttctgtt cgccatctgc ttctcttgtc tggcggctca cgtctttgcc   420

ctcaacttcc tggcccggaa gaaccacggg ccccgggget gggtgatctt cactgtggct   480

ctgctgctga ccctggtaga ggtcatcatc aatacagagt ggctgatcat caccctggtt   540

cggggcagtg gcgagggcgg ccctcagggc aacagcagcg caggctgggc cgtggcctcc   600

ccctgtgcca tcgccaacat ggactttgtc atggcactca tctacgtcat gctgctgctg   660

ctgggtgcct tcctgggggc ctggcccgcc ctgtgtggcc gctacaagcg ctggcgtaag   720

catggggtct ttgtgctcct caccacagcc acctccgttg ccatatgggt ggtgtggatc   780

gtcatgtata cttacggcaa caagcagcac aacagtccca cctgggatga ccccacgctg   840

gccatcgccc tcgccgccaa tgcctgggcc ttcgtcctct tctacgtcat ccccgaggtc   900

tcccaggtga ccaagtccag cccagagcaa agctaccagg gggacatgta ccccacccgg   960

```
ggcgtgggct atgagaccat cctgaaagag cagaagggtc agagcatgtt cgtggagaac      1020

aaggcctttt ccatggatga gccggttgca gctaagaggc cggtgtcacc atacagcggg      1080

tacaatgggc agctgctgac cagtgtgtac cagcccactg agatggccct gatgcacaaa      1140

gttccgtccg aaggagctta cgacatcatc ctcccacggg ccaccgccaa cagccaggtg      1200

atgggcagtg ccaactcgac cctgcgggct gaagacatgt actcggccca gagccaccag      1260

gcggccacac cgccgaaaga cggcaagaac tctcaggtct ttagaaaccc ctacgtgtgg      1320

gac                                                                    1323
```

<210> 106

<211> 795

<212> DNA

<213> Homo sapiens

<400> 106

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atggccgctg ccgtcccgaa gaggatgagg gggccagcac aagcgaaact gctgcccggg       60

tcggccatcc aagcccttgt ggggttggcg cggccgctgg tcttggcgct cctgcttgtg      120

tccgccgctc tatccagtgt tgtatcacgg actgattcac cgagcccaac cgtactcaac      180

tcacatattt ctaccccaaa tgtgaatgct ttaacacatg aaaaccaaac caaaccttct      240

atttcccaaa tcagcaccac cctccctccc acgacgagta ccaagaaaag tggaggagca      300

tctgtggtcc ctcatccctc gcctactcct ctgtctcaag aggaagctga taacaatgaa      360

gatcctagta tagaggagga ggatcttctc atgctgaaca gttctccatc cacagccaaa      420

gacactctag acaatggcga ttatggagaa ccagactatg actggaccac gggccccagg      480

gacgacgacg agtctgatga caccttggaa gaaaacaggg gttacatgga aattgaacag      540

tcagtgaaat cttttaagat gccatcctca aatatagaag aggaagacag ccatttcttt      600

tttcatctta ttattttttgc tttttgcatt gctgttgttt acattacata tcacaacaaa      660

aggaagattt ttcttctggt tcaaagcagg aaatggcgtg atggcctttg ttccaaaaca      720
```

gtggaatacc atcgcctaga tcagaatgtt aatgaggcaa tgccttcttt gaagattacc   780

aatgattata ttttt   795

<210> 107

<211> 624

<212> DNA

<213> Homo sapiens

<400> 107

atgctggggc tgctggtggc gttgctggcc ctggggctcg ctgtctttgc gctgctggac   60

gtctggtacc tggtgcgcct tccgtgcgcc gtgctgcgcg cgcgcctgct gcagccgcgc   120

gtccgtgacc tgctagctga gcagcgcttc ccgggccgcg tgctgccctc ggacttggac   180

ctgctgttgc acatgaacaa cgcgcgctac ctgcgcgagg ccgactttgc gcgcgtcgcg   240

cacctgaccc gctgcggggt gctcggggcg ctgagggagt tgcgggcgca cacggtgctg   300

gcggcctcgt gcgcgcgcca ccgccgctcg ctgcgcctgc tggagccctt cgaggtgcgc   360

acccgcctgc tgggctggga cgaccgcgcg ttctacctgg aggcgcgctt tgtcagcctg   420

cgggacggtt tcgtgtgcgc gctgctgcgc ttccggcagc acctgctggg cacctcaccc   480

gagcgcgtcg tgcagcacct gtgccagcgc agggtggagc ccctgagct gcccgctgat   540

ctgcagcact ggatctccta caacgaggcc agcagccagc tgctccgcat ggagagtggg   600

ctcagtgatg tcaccaagga ccag   624

<210> 108

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 108

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atggcgtggc ggcggcgcga agccagcgtc ggggctcgcg gcgtgttggc tctggcgttg    60

ctcgccctgg ccctgtgcgt gcccggggcc cggggccggg ctctcgagtg gttctcggcc   120

gtggtaaaca tcgagtacgt ggacccgcag accaacctga cggtgtggag cgtctcggag   180

agtggccgct tcggcgacag ctcgcccaag gagggcgcgc atggcctggt gggcgtcccg   240

tgggcgcccg gcggagacct cgagggctgc gcgcccgaca cgcgcttctt cgtgcccgag   300

cccggcggcc gaggggccgc gccctgggtc gccctggtgg ctcgtggggg ctgcaccttc   360

aaggacaagg tgctggtggc ggcgcggagg aacgcctcgg ccgtcgtcct ctacaatgag   420

gagcgctacg ggaacatcac cttgcccatg tctcacgcgg aacaggaaa tatagtggtc   480

attatgatta gctatccaaa aggaagagaa attttggagc tggtgcaaaa aggaattcca   540

gtaacgatga ccataggggt tggcacccgg catgtacagg agttcatcag cggtcagtct   600

gtggtgtttg tggccattgc cttcatcacc atgatgatta tctcgttagc ctggctaata   660

ttttactata tacagcgttt cctatatact ggctctcaga ttggaagtca gagccataga   720

aaagaaacta agaaagttat tggccagctt ctacttcata ctgtaaagca tggagaaaag   780

ggaattgatg ttgatgctga aaattgtgca gtgtgtattg aaaatttcaa agtaaaggat   840

attattagaa ttctgccatg caagcatatt tttcatagaa tatgcattga cccatggctt   900

ttggatcacc gaacatgtcc aatgtgtaaa cttgatgtca tcaaagccct aggatattgg   960

ggagagcctg gggatgtaca ggagatgcct gctccagaat ctcctcctgg aagggatcca  1020

gctgcaaatt tgagtctagc tttaccagat gatgacggaa gtgatgagag cagtccacca  1080

tcagcctccc ctgctgaatc tgagccacag tgtgatccca gctttaaagg agatgcagga  1140

gaaaatacgg cattgctaga agccggcagg agtgactctc ggcatggagg acccatctcc  1200
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<210> 109

<211> 576

<212> DNA

<213> Homo sapiens

<400> 109

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ggatgtgttt tccagagcac agaagacaaa tgtatattca agatagactg gactctgtca   180

ccaggagagc acgccaagga cgaatatgtg ctatactatt actccaatct cagtgtgcct   240

attgggcgct tccagaaccg cgtacacttg atggggggaca acttatgcaa tgatggctct   300

ctcctgctcc aagatgtgca agaggctgac cagggaacct atatctgtga aatccgcctc   360

aaagggagga gccaggtgtt caagaaggcg gtggtactgc atgtgcttcc agaggagccc   420

aaagagctca tggtccatgt gggtggattg attcagatgg gatgtgtttt ccagagcaca   480

gaagtgaaac acgtgaccaa ggtagaatgg atattttcag acggcgcgc aaaggtaaca   540

aggaggaaac atcactgtgt tagagaaggc tctggc   576

<210> 110

<211> 780

<212> DNA

<213> Homo sapiens

<400> 110

atggcggggt cgccgctgct ctgggggccg cgggccgggg gcgtcggcct tttggtgctg   60

ctgctgctcg gcctgtttcg gccgccccccc gcgctctgcg cgcggccggt aaaggagccc   120

cgcggcctaa gcgcagcgtc tccgcccttg gctgagactg cgctcctcg ccgcttccgg   180

cggtcagtgc cccgaggtga ggcggcgggg gcggtgcagg agctggcgcg ggcgctggcg   240

catctgctgg aggccgaacg tcaggagcgg gcgcgggccg aggcgcagga ggctgaggat   300

cagcaggcgc gcgtcctggc gcagctgctg cgcgtctggg gcgcccccccg caactctgat   360

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ctccgcgccc gccttgaccc tgccgccctc gcagcccagc ttgtccccgc gcccgtcccc   480

gccgcggcgc tccgaccccg gcccccggtc tacgacgacg gccccgcggg cccggatgct   540

gaggaggcag gcgacgagac acccgacgtg gaccccgagc tgttgaggta cttgctggga   600

cggattcttg cgggaagcgc ggactccgag ggggtggcag ccccgcgccg cctccgccgt   660

gccgccgacc acgatgtggg ctctgagctg cccctgagg gcgtgctggg ggcgctgctg   720

cgtgtgaaac gcctagagac cccggcgccc caggtgcctg cacgccgcct cttgccaccc   780

<210> 111

<211> 1633

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (68)... (1498)

<400> 111

acaaccggct ggggtccttg cgcgccgcgg ctcagggagg agcaccgact gcgccgcacc   60

ctgagag atg gtt ggt gcc atg tgg aag gtg att gtt tcg ctg gtc ctg   109
        Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu
        1   5   10

ttg atg cct ggc ccc tgt gat ggg ctg ttt cgc tcc cta tac aga agt   157
Leu Met Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser
15   20   25   30

gtt tcc atg cca cct aag gga gac tca gga cag cca tta ttt ctc acc   205
Val Ser Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr
                35   40   45

cct tac att gaa gct ggg aag atc caa aaa gga aga gaa ttg agt ttg   253

Pro Tyr Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu

                    50   55   60

gtc ggc cct ttc cca gga ctg aac atg aag agt tat gcc ggc ttc ctc   301

Val Gly Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu

                    65   70   75

acc gtg aat aag act tac aac agc aac ctc ttc ttc tgg ttc ttc cca   349

Thr Val Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro

                80   85   90

gct cag ata cag cca gaa gat gcc cca gta gtt ctc tgg cta cag ggt   397

Ala Gln Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly

95   100   105   110

ggg ccg gga ggt tca tcc atg ttt gga ctc ttt gtg gaa cat ggg cct   445

Gly Pro Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro

                    115   120   125

tat gtt gtc aca agt aac atg acc ttg cgt gac aga gac ttc ccc tgg   493

Tyr Val Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp

                    130   135   140

acc aca acg ctc tcc atg ctt tac att gac aat cca gtg ggc aca ggc   541

Thr Thr Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly

                    145   150   155

ttc agt ttt act gat gat acc cac gga tat gca gtc aat gag gac gat   589

Phe Ser Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp

                160   165   170

gta gca cgg gat tta tac agt gca cta att cag ttt ttc cag ata ttt   637

Val Ala Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe

	175				180				185				190		
cct	gaa	tat	aaa	aat	aat	gac	ttt	tat	gtc	act	ggg	gag	tct	tat	gca	685
Pro	Glu	Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala

				195					200					205	
ggg	aaa	tat	gtg	cca	gcc	att	gca	cac	ctc	atc	cat	tcc	ctc	aac	cct	733
Gly	Lys	Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro

				210					215					220	
gtg	aga	gag	gtg	aag	atc	aac	ctg	aac	gga	att	gct	att	gga	gat	gga	781
Val	Arg	Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly

				225					230					235	
tat	tct	gat	ccc	gaa	tca	att	ata	ggg	ggc	tat	gca	gaa	ttc	ctg	tac	829
Tyr	Ser	Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr

	240				245				250						
caa	att	ggc	ttg	ttg	gat	gag	aag	caa	aaa	aag	tac	ttc	cag	aag	cag	877
Gln	Ile	Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln

255				260					265					270	
tgc	cat	gaa	tgc	ata	gaa	cac	atc	agg	aag	cag	aac	tgg	ttt	gag	gcc	925
Cys	His	Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala

				275					280					285	
ttt	gaa	ata	ctg	gat	aaa	cta	cta	gat	ggc	gac	tta	aca	agt	gat	cct	973
Phe	Glu	Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro

				290					295					300	
tct	tac	ttc	cag	aat	gtt	aca	gga	tgt	agt	aat	tac	tat	aac	ttt	ttg	1021
Ser	Tyr	Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu

| | | | | 305 | | | | | 310 | | | | | 315 | |

```
cgg tgc acg gaa cct gag gat cag ctt tac tat gtg aaa ttt ttg tca      1069
Arg Cys Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser
    320                 325                 330

ctc cca gag gtg aga caa gcc atc cac gtg ggg aat cag act ttt aat      1117
Leu Pro Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn
335                 340                 345                 350

gat gga act ata gtt gaa aag tac ttg cga gaa gat aca gta cag tca      1165
Asp Gly Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser
                355                 360                 365

gtt aag cca tgg tta act gaa atc atg aat aat tat aag gtt ctg atc      1213
Val Lys Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile
            370                 375                 380

tac aat ggc caa ctg gac atc atc gtg gca gct gcc ctg aca gag cac      1261
Tyr Asn Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu His
            385                 390                 395

tcc ttg atg ggc atg gac tgg aaa gga tcc cag gaa tac aag aag gca      1309
Ser Leu Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala
    400                 405                 410

gaa aaa aaa gtt tgg aag atc ttt aaa tct gac agt gaa gtg gct ggt      1357
Glu Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly
415                 420                 425                 430

tac atc cgg caa gcg ggt gac ttc cat cag gta att att cga ggt gga      1405
Tyr Ile Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly
                435                 440                 445

gga cat att tta ccc tat gac cag cct ctg aga gct ttt gac atg att      1453
```

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Gly His Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile
            450              455              460

aat cga ttc att tat gga aaa gga tgg gat cct tat gtt gga taaac      1500
Asn Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
            465              470              475

taccttccca aaagagaaca tcagaggttt tcattgctga aaagaaaatc gtaaaaacag  1560

aaaatgtcat aggaataaaa aaattatctt ttcatatctg caagattttt ttcatcaata  1620

aaaattatcc ttg                                                     1633
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<210> 112

<211> 1095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (192)... (872)

<400> 112

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ctttaaaatg tcattggtaa accatacttg atcctaaatt cctgtacttc ctcaggccat    60

ccgagcatga aacgctgtca cctacccaca tccgctggct gtgacgcttg tcaaagtgtt   120

ctctatcggc tgcatgccta gaccaccaaa gcgttctgac cggacagtgt cactggagaa   180

ggcggcgcga c atg tcc agg gcg cag atc tgg gct ctg gtg tct ggt gtc   230
            Met Ser Arg Ala Gln Ile Trp Ala Leu Val Ser Gly Val
             1               5                  10

gga ggg ttt gga gct ctc gtt gct gct acc acg tcc aat gag tgg aaa    278
Gly Gly Phe Gly Ala Leu Val Ala Ala Thr Thr Ser Asn Glu Trp Lys
```

```
            15                    20                    25
gtg acc acg cga gcc tcc tcg gtg ata aca gcc act tgg gtt tac cag      326
Val Thr Thr Arg Ala Ser Ser Val Ile Thr Ala Thr Trp Val Tyr Gln

     30                    35                    40                    45
ggt ctg tgg atg aac tgc gca ggt aac gcg ttg ggt tct ttc cat tgc      374
Gly Leu Trp Met Asn Cys Ala Gly Asn Ala Leu Gly Ser Phe His Cys

                    50                    55                    60
cga ccg cat ttt act atc ttc aaa gta gca ggt tat ata cag gca tgt      422
Arg Pro His Phe Thr Ile Phe Lys Val Ala Gly Tyr Ile Gln Ala Cys

                    65                    70                    75
aga gga ctt atg atc gct gct gtc agc ctg ggc ttc ttt ggt tcc ata      470
Arg Gly Leu Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile

               80                    85                    90
ttt gcg ctc ttt gga atg aag tgt acc aaa gtc gga ggc tcc gat aaa      518
Phe Ala Leu Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys

     95                    100                   105
gcc aaa gct aaa att gct tgt ttg gct ggg att gta ttc ata ctg tca      566
Ala Lys Ala Lys Ile Ala Cys Leu Ala Gly Ile Val Phe Ile Leu Ser
110                   115                   120                   125
ggg ctg tgc tca atg act gga tgt tcc cta tat gca aac aaa atc aca      614
Gly Leu Cys Ser Met Thr Gly Cys Ser Leu Tyr Ala Asn Lys Ile Thr

                    130                   135                   140
acg gaa ttc ttt gat cct ctc ttt gtt gag caa aag tat gaa tta gga      662
Thr Glu Phe Phe Asp Pro Leu Phe Val Glu Gln Lys Tyr Glu Leu Gly

          145                   150                   155
```

```
gcc gct ctg ttt att gga tgg gca gga gcc tca ctg tgc ata att ggt        710
Ala Ala Leu Phe Ile Gly Trp Ala Gly Ala Ser Leu Cys Ile Ile Gly
            160                 165                 170

ggt gtc ata ttt tgc ttt tca ata tct gac aac aac aaa aca ccc aga        758
Gly Val Ile Phe Cys Phe Ser Ile Ser Asp Asn Asn Lys Thr Pro Arg
        175                 180                 185

tac aca tac aac ggg gcc aca tct gtc atg tct tct cgg aca aag tat        806
Tyr Thr Tyr Asn Gly Ala Thr Ser Val Met Ser Ser Arg Thr Lys Tyr
190                 195                 200                 205

cat ggt gga gaa gat ttt aaa aca aca aac cct tca aaa cag ttt gat        854
His Gly Gly Glu Asp Phe Lys Thr Thr Asn Pro Ser Lys Gln Phe Asp
                210                 215                 220

aaa aat gct tat gtc t aaaagagctc gcgggcaagc tgcctcttga               900
Lys Asn Ala Tyr Val
                225

gtttgttata aaagcgaact gttcacaaaa tgatcccatc aaggccctcc cataattaac    960
actcaaaact atttttaaaa tatgcatttg aagcatctgt tgattgtatg gatgtaagtg    1020
ttcttacata gttagttata tactaatcat tttctgttgt ggctttctat aaaaaataaa    1080
cagtttattt acagg                                                     1095
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<210> 113

<211> 1602

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (34)...(951)

<400> 113

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tttgtcaggt ggtggaggaa aaggcgctcc gtc atg ggg atc cag acg agc ccc        54
                                      Met Gly Ile Gln Thr Ser Pro
                                       1               5
gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act ctg ctc ggc ctg       102
Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu
         10              15              20
gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg cct cag gtc act       150
Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr
     25              30              35
ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg cta gac aag acg       198
Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr
 40              45              50              55
act gtg agc cac aac acc aag agg ttc cgc ttt gcc ctg ccc acc gcc       246
Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala
             60              65              70
cac cac act ctg ggg ctg cct gtg ggc aaa cat atc tac ctc tcc acc       294
His His Thr Leu Gly Leu Pro Val Gly Lys His Ile Tyr Leu Ser Thr
             75              80              85
cga att gat ggc agc ctg gtc atc agg cca tac act cct gtc acc agt       342
Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr Pro Val Thr Ser
             90              95              100
gat gag gat caa ggc tat gtg gat ctt gtc atc aag gtc tac ctg aag       390
```

Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Ile Lys Val Tyr Leu Lys

105   110   115

ggt gtg cac ccc aaa ttt cct gag gga ggg aag atg tct cag tac ctg   438

Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met Ser Gln Tyr Leu

120   125   130   135

gat agc ctg aag gtt ggg gat gtg gtg gag ttt cgg ggg cca agc ggg   486

Asp Ser Leu Lys Val Gly Asp Val Val Glu Phe Arg Gly Pro Ser Gly

          140   145   150

ttg ctc act tac act gga aaa ggg cat ttt aac att cag ccc aac aag   534

Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile Gln Pro Asn Lys

          155   160   165

aaa tct cca cca gaa ccc cga gtg gcg aag aaa ctg gga atg att gcc   582

Lys Ser Pro Pro Glu Pro Arg Val Ala Lys Lys Leu Gly Met Ile Ala

          170   175   180

ggc ggg aca gga atc acc cca atg cta cag ctg atc cgg gcc atc ctg   630

Gly Gly Thr Gly Ile Thr Pro Met Leu Gln Leu Ile Arg Ala Ile Leu

          185   190   195

aaa gtc cct gaa gat cca acc cag tgc ttt ctg ctt ttt gcc aac cag   678

Lys Val Pro Glu Asp Pro Thr Gln Cys Phe Leu Leu Phe Ala Asn Gln

200   205   210   215

aca gaa aag gat atc atc ttg cgg gag gac tta gag gaa ctg cag gcc   726

Thr Glu Lys Asp Ile Ile Leu Arg Glu Asp Leu Glu Glu Leu Gln Ala

          220   225   230

cgc tat ccc aat cgc ttt aag ctc tgg ttc act ctg gat cat ccc cca   774

Arg Tyr Pro Asn Arg Phe Lys Leu Trp Phe Thr Leu Asp His Pro Pro

```
          235                   240                   245
aaa gat tgg gcc tac agc aag ggc ttt gtg act gcc gac atg atc cgg        822
Lys Asp Trp Ala Tyr Ser Lys Gly Phe Val Thr Ala Asp Met Ile Arg

          250                   255                   260
gaa cac ctg ccc gct cca ggg gat gat gtg ctg gta ctg ctt tgt ggg        870
Glu His Leu Pro Ala Pro Gly Asp Asp Val Leu Val Leu Leu Cys Gly

          265                   270                   275
cca ccc cca atg gtg cag ctg gcc tgc cat ccc aac ttg gac aaa ctg        918
Pro Pro Pro Met Val Gln Leu Ala Cys His Pro Asn Leu Asp Lys Leu

280                   285                   290                   295
ggc tac tca caa aag atg cga ttc acc tac tg agcatcctcc agcttccctg        970
Gly Tyr Ser Gln Lys Met Arg Phe Thr Tyr

                    300                   305
gtgctgttcg ctgcagttgt tccccatcag tactcaagca ctataagcct tagattcctt      1030
tcctcagagt ttcaggtttt ttcagttaca tctagagctg aaatctggat agtacctgca      1090
ggaacaatat tcctgtagcc atggaagagg gccaaggctc agtcactcct tggatggcct      1150
cctaaatctc cccgtggcaa caggtccagg agaggcccat ggagcagtct cttccatgga      1210
gtaagaagga agggagcatg tacgcttggt ccaagattgg ctagttcctt gatagcatct      1270
tactctcacc ttctttgtgt ctgtgatgaa aggaacagtc tgtgcaatgg gttttactta      1330
aacttcactg ttcaacctat gagcaaatct gtatgtgtga gtataagttg agcatagcat      1390
acttccagag gtggtcttat ggagatggca agaaaggagg aaatgatttc ttcagatctc      1450
aaaggagtct gaaatatcat atttctgtgt gtgtctctct cagcccctgc ccaggctaga      1510
gggaaacagc tactgataat cgaaaactgc tgtttgtggc aggaacccct ggctgtgcaa      1570
ataaatgggg ctgaggcccc tgtgtgatat tg                                    1602
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<210> 114

<211> 897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (99)...(782)

<400> 114

agtcctccca aagtacttgt gtccgggtgg tggactggat tcgctgcgga gccctggaag   60

ctgcctttcc ttctccctgt gcttaaccag aggtgccc atg ggt tgg aca atg   113
                                         Met Gly Trp Thr Met
                                          1   5

agg ctg gtc aca gca gca ctg tta ctg ggt ctc atg atg gtg gtc act   161
Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu Met Met Val Val Thr
              10   15   20

gga gac gag gat gag aac agc ccg tgt gcc cat gag gcc ctc ttg gac   209
Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His Glu Ala Leu Leu Asp
          25   30   35

gag gac acc ctc ttt tgc cag ggc ctt gaa gtt ttc tac cca gag ttg   257
Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val Phe Tyr Pro Glu Leu
      40   45   50

ggg aac att ggc tgc aag gtt gtt cct gat tgt aac aac tac aga cag   305
Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys Asn Asn Tyr Arg Gln
  55   60   65

aag atc acc tcc tgg atg gag ccg ata gtc aag ttc ccg ggg gcc gtg   353

Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys Phe Pro Gly Ala Val
70   75   80   85

gac ggc gca acc tat atc ctg gtg atg gtg gat cca gat gcc cct agc   401
Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp Pro Asp Ala Pro Ser
              90   95   100

aga gca gaa ccc aga cag aga ttc tgg aga cat tgg ctg gta aca gat   449
Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His Trp Leu Val Thr Asp
              105   110   115

atc aag ggc gcc gac ctg aag aaa ggg aag att cag ggc cag gag tta   497
Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile Gln Gly Gln Glu Leu
             120   125   130

tca gcc tac cag gct ccc tcc cca ccg gca cac agt ggc ttc cat cgc   545
Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His Ser Gly Phe His Arg
             135   140   145

tac cag ttc ttt gtc tat ctt cag gaa gga aaa gtc atc tct ctc ctt   593
Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys Val Ile Ser Leu Leu
150   155   160   165

ccc aag gaa aac aaa act cga ggc tct tgg aaa atg gac aga ttt ctg   641
Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys Met Asp Arg Phe Leu
             170   175   180

aac cgt ttc cac ctg ggc gaa cct gaa gca agc acc cag ttc atg acc   689
Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser Thr Gln Phe Met Thr
             185   190   195

cag aac tac cag gac tca cca acc ctc cag gct ccc aga gaa agg gcc   737
Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala Pro Arg Glu Arg Ala

```
            200                 205                 210
agc gag ccc aag cac aaa aac cag gcg gag ata gct gcc tgc t                780
Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile Ala Ala Cys

              215                 220                 225
agatagccgg ctttgccatc cgggcatgtg gccacactgc ccaccaccga cgatgtgggt       840

atggaacccc ctctggatac agaacccctt cttttccaaa taaaaaaaaa atcatcc          897
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<210> 115

<211> 1866

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (142)... (1467)

<400> 115

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gcccgcatgc gggggcgtgg cagtcaacag caacaaccca cacgccggca gggccagaaa        60

ctcccatctc cctcaccagc cggaaagtac gagtcggctc agcctggagg gacccaacca       120

gagcctggcc tgggagccag g atg gcc atc cac aaa gcc ttg gtg atg tgc         171
                        Met Ala Ile His Lys Ala Leu Val Met Cys
                         1               5                  10

ctg gga ctg cct ctc ttc ctg ttc cca ggg gcc tgg gcc cag ggc cat        219
Leu Gly Leu Pro Leu Phe Leu Phe Pro Gly Ala Trp Ala Gln Gly His
              15                  20                  25

gtc cca ccc ggc tgc agc caa ggc ctc aac ccc ctg tac tac aac ctg        267
Val Pro Pro Gly Cys Ser Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu
```

```
                30                    35                    40
tgt gac cgc tct ggg gcg tgg ggc atc gtc ctg gag gcc gtg gct ggg        315
Cys Asp Arg Ser Gly Ala Trp Gly Ile Val Leu Glu Ala Val Ala Gly
                45                    50                    55
gcg ggc att gtc acc acg ttt gtg ctc acc atc atc ctg gtg gcc agc        363
Ala Gly Ile Val Thr Thr Phe Val Leu Thr Ile Ile Leu Val Ala Ser
                60                    65                    70
ctc ccc ttt gtg cag gac acc aag aaa cgg agc ctg ctg ggg acc cag        411
Leu Pro Phe Val Gln Asp Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln
    75                    80                    85                    90
gta ttc ttc ctt ctg ggg acc ctg ggc ctc ttc tgc ctc gtg ttt gcc        459
Val Phe Phe Leu Leu Gly Thr Leu Gly Leu Phe Cys Leu Val Phe Ala
                    95                    100                   105
tgt gtg gtg aag ccc gac ttc tcc acc tgt gcc tct cgg cgc ttc ctc        507
Cys Val Val Lys Pro Asp Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu
                110                   115                   120
ttt ggg gtt ctg ttc gcc atc tgc ttc tct tgt ctg gcg gct cac gtc        555
Phe Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Ala Ala His Val
                125                   130                   135
ttt gcc ctc aac ttc ctg gcc cgg aag aac cac ggg ccc cgg ggc tgg        603
Phe Ala Leu Asn Phe Leu Ala Arg Lys Asn His Gly Pro Arg Gly Trp
                140                   145                   150
gtg atc ttc act gtg gct ctg ctg ctg acc ctg gta gag gtc atc atc        651
Val Ile Phe Thr Val Ala Leu Leu Leu Thr Leu Val Glu Val Ile Ile
    155                   160                   165                   170
```

aat aca gag tgg ctg atc atc acc ctg gtt cgg ggc agt ggc gag ggc   699
Asn Thr Glu Trp Leu Ile Ile Thr Leu Val Arg Gly Ser Gly Glu Gly
              175   180   185

ggc cct cag ggc aac agc agc gca ggc tgg gcc gtg gcc tcc ccc tgt   747
Gly Pro Gln Gly Asn Ser Ser Ala Gly Trp Ala Val Ala Ser Pro Cys
              190   195   200

gcc atc gcc aac atg gac ttt gtc atg gca ctc atc tac gtc atg ctg   795
Ala Ile Ala Asn Met Asp Phe Val Met Ala Leu Ile Tyr Val Met Leu
              205   210   215

ctg ctg ctg ggt gcc ttc ctg ggg gcc tgg ccc gcc ctg tgt ggc cgc   843
Leu Leu Leu Gly Ala Phe Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg
              220   225   230

tac aag cgc tgg cgt aag cat ggg gtc ttt gtg ctc ctc acc aca gcc   891
Tyr Lys Arg Trp Arg Lys His Gly Val Phe Val Leu Leu Thr Thr Ala
235   240   245   250

acc tcc gtt gcc ata tgg gtg gtg tgg atc gtc atg tat act tac ggc   939
Thr Ser Val Ala Ile Trp Val Val Trp Ile Val Met Tyr Thr Tyr Gly
              255   260   265

aac aag cag cac aac agt ccc acc tgg gat gac ccc acg ctg gcc atc   987
Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile
              270   275   280

gcc ctc gcc gcc aat gcc tgg gcc ttc gtc ctc ttc tac gtc atc ccc   1035
Ala Leu Ala Ala Asn Ala Trp Ala Phe Val Leu Phe Tyr Val Ile Pro
              285   290   295

gag gtc tcc cag gtg acc aag tcc agc cca gag caa agc tac cag ggg   1083

236/307

```
            Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly
                300                 305                 310

gac atg tac ccc acc cgg ggc gtg ggc tat gag acc atc ctg aaa gag        1131
Asp Met Tyr Pro Thr Arg Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu
315                 320                 325     ·           330

cag aag ggt cag agc atg ttc gtg gag aac aag gcc ttt tcc atg gat        1179
Gln Lys Gly Gln Ser Met Phe Val Glu Asn Lys Ala Phe Ser Met Asp
                335                 340                 345

gag ccg gtt gca gct aag agg ccg gtg tca cca tac agc ggg tac aat        1227
Glu Pro Val Ala Ala Lys Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn
                350                 355                 360

ggg cag ctg ctg acc agt gtg tac cag ccc act gag atg gcc ctg atg        1275
Gly Gln Leu Leu Thr Ser Val Tyr Gln Pro Thr Glu Met Ala Leu Met
                365                 370                 375

cac aaa gtt ccg tcc gaa gga gct tac gac atc atc ctc cca cgg gcc        1323
His Lys Val Pro Ser Glu Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala
                380                 385                 390

acc gcc aac agc cag gtg atg ggc agt gcc aac tcg acc ctg cgg gct        1371
Thr Ala Asn Ser Gln Val Met Gly Ser Ala Asn Ser Thr Leu Arg Ala
395                 400                 405                 410

gaa gac atg tac tcg gcc cag agc cac cag gcg gcc aca ccg ccg aaa        1419
Glu Asp Met Tyr Ser Ala Gln Ser His Gln Ala Ala Thr Pro Pro Lys
                415                 420                 425

gac ggc aag aac tct cag gtc ttt aga aac ccc tac gtg tgg gac          1464
Asp Gly Lys Asn Ser Gln Val Phe Arg Asn Pro Tyr Val Trp Asp
```

```
                    430                 435                 440

tgagtc agcggtggcg aggagaggcg gtcggatttg gggagggccc tgaggacctg        1520

gccccgggca agggactctc caggctcctc ctcccccctgg caggcccagc aacatgtgcc   1580

ccagatgtgg aagggcctcc ctctctgcca gtgtttgggt gggtgtcatg ggtgtcccca   1640

cccactcctc agtgtttgtg gagtcgagga gccaacccca gcctcctgcc aggatcacct   1700

cggcggtcac actccagcca aatagtgttc tcggggtggt ggctgggcag cgcctatgtt   1760

tctctggaga ttcctgcaac ctcaagagac ttcccaggcg ctcaggcctg gatcttgctc   1820

ctctgtgagg aacaagggtg cctaataaat acatttctgc tttatt               1866
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<210> 116

<211> 2198

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)... (847)

<400> 116

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aaaatggcgt agagcctagc aacagcgcag gctcccagcc gagtccgtt atg gcc        55
                                                       Met Ala
                                                         1

gct gcc gtc ccg aag agg atg agg ggg cca gca caa gcg aaa ctg ctg     103
Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys Leu Leu
      5                 10                  15

ccc ggg tcg gcc atc caa gcc ctt gtg ggg ttg gcg cgg ccg ctg gtc    151
Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro Leu Val
```

```
              20                    25                    30
ttg gcg ctc ctg ctt gtg tcc gcc gct cta tcc agt gtt gta tca cgg      199
Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val Ser Arg
  35                    40                    45                    50
act gat tca ccg agc cca acc gta ctc aac tca cat att tct acc cca      247
Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser Thr Pro
                      55                    60                    65
aat gtg aat gct tta aca cat gaa aac caa acc aaa cct tct att tcc      295
Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser Ile Ser
                      70                    75                    80
caa atc agc acc acc ctc cct ccc acg acg agt acc aag aaa agt gga      343
Gln Ile Ser Thr Thr Leu Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly
              85                    90                    95
gga gca tct gtg gtc cct cat ccc tcg cct act cct ctg tct caa gag      391
Gly Ala Ser Val Val Pro His Pro Ser Pro Thr Pro Leu Ser Gln Glu
              100                   105                   110
gaa gct gat aac aat gaa gat cct agt ata gag gag gag gat ctt ctc      439
Glu Ala Asp Asn Asn Glu Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu
115                   120                   125                   130
atg ctg aac agt tct cca tcc aca gcc aaa gac act cta gac aat ggc      487
Met Leu Asn Ser Ser Pro Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly
                      135                   140                   145
gat tat gga gaa cca gac tat gac tgg acc acg ggc ccc agg gac gac      535
Asp Tyr Gly Glu Pro Asp Tyr Asp Trp Thr Thr Gly Pro Arg Asp Asp
              150                   155                   160
```

```
gac gag tct gat gac acc ttg gaa gaa aac agg ggt tac atg gaa att      583
Asp Glu Ser Asp Asp Thr Leu Glu Glu Asn Arg Gly Tyr Met Glu Ile
        165                 170                 175

gaa cag tca gtg aaa tct ttt aag atg cca tcc tca aat ata gaa gag      631
Glu Gln Ser Val Lys Ser Phe Lys Met Pro Ser Ser Asn Ile Glu Glu
        180                 185                 190

gaa gac agc cat ttc ttt ttt cat ctt att att ttt gct ttt tgc att      679
Glu Asp Ser His Phe Phe Phe His Leu Ile Ile Phe Ala Phe Cys Ile
195                 200                 205                 210

gct gtt gtt tac att aca tat cac aac aaa agg aag att ttt ctt ctg      727
Ala Val Val Tyr Ile Thr Tyr His Asn Lys Arg Lys Ile Phe Leu Leu
                215                 220                 225

gtt caa agc agg aaa tgg cgt gat ggc ctt tgt tcc aaa aca gtg gaa      775
Val Gln Ser Arg Lys Trp Arg Asp Gly Leu Cys Ser Lys Thr Val Glu
                230                 235                 240

tac cat cgc cta gat cag aat gtt aat gag gca atg cct tct ttg aag      823
Tyr His Arg Leu Asp Gln Asn Val Asn Glu Ala Met Pro Ser Leu Lys
        245                 250                 255

att acc aat gat tat att ttt taaagc actgtgattt gaatttgctt            870
Ile Thr Asn Asp Tyr Ile Phe
        260                 265

atgtaatttt atttgcttga ctttttatat gatattgtgc aaatgtttgc cataggcaat   930

tggtacttaa atgagaggtg agtctctctt ttgccttggt gctttggaaa ttaaatgtca   990

caaacgagta tataatttttt tatctgtact tttagagctg agtttaatca ggtgtccaaa  1050

atgtgagtta aacattacct tatatttaca ctgttagttt ttattgtttt agatttatta  1110
```

```
tgcttcttct ggaagtatta gtgatgctac ttttaaaaga tcccaaactt gtaactaaat   1170

tctgacatat ctgttactgc tgactcacat tcattctccg ccattcaaat actatttttt   1230

atccacattt tttttgttc ccaaactgta atgtacaagg atatgtgtga taatgctttg   1290

gatttgagta atatttttt ttcttccaag aaaactgctt tggatatttt tagataattt   1350

aaacataatt taggataatg atattgctca atctgaccac aatttaggt aaaacattaa   1410

atgtgtcaag aaatcttggc aacagagact ctgcagcttg cagtggacat agataaaatg   1470

ttacagagat actattttt tggttggaat tactatatta aatttagaag cagaaactgg   1530

taaaatgtta aatacatgta caattgcttt tagttagcaa ttgattgtag catgggttcc   1590

tccaaggttt caagcaatgg gcagagttta aaattatatc agattcgttt acttcgttta   1650

ttattttaca gtaaatttga ataaatctta ggggtcatta tcacttaaat aatactgtac   1710

ctaggtcttt caaattaaaa ttatacctga atgaagttgt ttgtatacat aaaggatatt   1770

tgtgtacaat tacctttttt cccccacact tgttttcttt gttttttgttt tttatggcaa   1830

ctggaaagta tttactatgg gattcattta tgtctgtctt tctatcataa agaattgatc   1890

aatatgtaaa tatgtgattt gaaccatggt tgacttacaa gtgtcactac agctttttag   1950

aaaacatagc cctaatatat gttaagcagg acccgggtga gccagtgggc ttgcgcttta   2010

tgtagagctg gaagaaggcc gtccatcctg tctcttgggc ggacagtgta ctttcctaat   2070

agggaaggga agcacaatgg aaatacccct gaaccgtttt attgcagtaa ttttttcat   2130

atctgaaact attatttaat attttgaata agattttaaa aaataaatgg caaagatata   2190

aatctatg                                                           2198
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<210> 117

<211> 2180

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (69)... (695)

<400> 117

aaccagcgcc gcggacaccg gcaccggcgc cacggactcc gcaggacccc gcgcccgccg   60

ccgccgct atg ctg ggg ctg ctg gtg gcg ttg ctg gcc ctg ggg ctc gct   110
         Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala
          1   5   10

gtc ttt gcg ctg ctg gac gtc tgg tac ctg gtg cgc ctt ccg tgc gcc   158
Val Phe Ala Leu Leu Asp Val Trp Tyr Leu Val Arg Leu Pro Cys Ala
 15   20   25   30

gtg ctg cgc gcg cgc ctg ctg cag ccg cgc gtc cgt gac ctg cta gct   206
Val Leu Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala
                  35   40   45

gag cag cgc ttc ccg ggc cgc gtg ctg ccc tcg gac ttg gac ctg ctg   254
Glu Gln Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu
                  50   55   60

ttg cac atg aac aac gcg cgc tac ctg cgc gag gcc gac ttt gcg cgc   302
Leu His Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg
                  65   70   75

gtc gcg cac ctg acc cgc tgc ggg gtg ctc ggg gcg ctg agg gag ttg   350
Val Ala His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu Leu
          80   85   90

cgg gcg cac acg gtg ctg gcg gcc tcg tgc gcg cgc cac cgc cgc tcg   398
Arg Ala His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg Ser
 95   100   105   110

```
ctg cgc ctg ctg gag ccc ttc gag gtg cgc acc cgc ctg ctg ggc tgg          446
Leu Arg Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp
            115                 120                 125

gac gac cgc gcg ttc tac ctg gag gcg cgc ttt gtc agc ctg cgg gac          494
Asp Asp Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp
            130                 135                 140

ggt ttc gtg tgc gcg ctg ctg cgc ttc cgg cag cac ctg ctg ggc acc          542
Gly Phe Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr
        145                 150                 155

tca ccc gag cgc gtc gtg cag cac ctg tgc cag cgc agg gtg gag ccc          590
Ser Pro Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro
        160                 165                 170

cct gag ctg ccc gct gat ctg cag cac tgg atc tcc tac aac gag gcc          638
Pro Glu Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala
175                 180                 185                 190

agc agc cag ctg ctc cgc atg gag agt ggg ctc agt gat gtc acc aag          686
Ser Ser Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys
            195                 200                 205

gac cag tgaccgcc accttcacac cgtctgccct ggccaccatc ctgggcctgg             740
Asp Gln

gggctgccca cagatgggca gtctcagcca tactctgttc cagctggagt agcctcctga        800

ccagcctggc ccaccctgct ccacccactg gcccccccca gttattgata cccctctgtg        860

ctgggctcca cgctaggcag aaggaggagt ggcattggca tcctgaccca gctctgccct        920

caaggtgggg atggatgggc aaaggagagt cctgcctggc cctacgatga ggccactcat        980

gtgggcctag gtaggggagg atggtgcctg gagcagaggg acccacaagt gcctcccgag        1040
```

```
cctagatcct ggctcggacc actgcaaggg ccgaggcagg gccagaccag agcatcctgg   1100

gtacaggcct gggctctcca gggcctgggc ctgattcagg tgcagtgggc actcctgaag   1160

ggtcagagcg gcatctgcca ggcagcccct ctggcttccg ctgaggtggt tgcaggcctg   1220

gggcagagcc tgggtggtca gaggccgggg ctagaggcag atggaaggga ggcatttgct   1280

gacagaggac ggggcacccg ggctcccact gcagtcggcc ttgcctcctc ctcctcctct   1340

acctccagtc aggctggacg ggagggtagc cttgtggctg agaggggtca gactaggtgg   1400

cacaggggct cctggaaaga cagcaggctt cctgctgggc gttcccttgt tggagggaat   1460

agagtggggg tgggactctg caggggtgtc cttgtccact cgcacccctc gccgcccacc   1520

agggccatgc tctgtgactt gggctgatcc ccacccttc tgggcctaca gcaccacagg   1580

ccgctgtacc cccttagagc tgcccctctc tggcctggcc ggcagacgtc ttcttaactc   1640

ctctgtcctc tatattcagc atgttccttg tcagctgctg ggccggccct gccttgcgct   1700

agcagagcct ctcctggcag cttctcaggt ctccctaatg gagacaccag gctactagga   1760

cactggctgg ggccaccccc tcctgcctaa tgcctcacct tacagctggg gaaactgagg   1820

cctggaatgg cccagagtca ccaaggcaaa gttggggctg gtcccagcct gaggctccag   1880

ctgatgccct cagctcccag agagggggtg ccccatctag ctgggtgcag gggtcactgc   1940

ttgtcagctc agggccctgt gcccgcttgc ctgttcccct acatctgtgc ctgcacatcc   2000

agaactgcct ccttgccgct gcctccagga agcccacctt gagccagagt caagggctgc   2060

agcactgccc gatagaacac gcccgccctc actgctgttc ttgccttaca gccaccatgg   2120

gaaagctgca acctttctgt tttatttaaa gaaagcccaa cattaaaggg ttttcattgc   2180
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<210> 118

<211> 1527

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)... (1305)

<400> 118

agtcttccag ggcggcggtg ggtgtccgct tctctctgct cttcgactgc accgcactcg   60

cgcgtgaccc tgactccccc tagtcagctc agcggtgctg cc atg gcg tgg cgg   114

               Met Ala Trp Arg

                  1

cgg cgc gaa gcc agc gtc ggg gct cgc ggc gtg ttg gct ctg gcg ttg   162

Arg Arg Glu Ala Ser Val Gly Ala Arg Gly Val Leu Ala Leu Ala Leu

5   10   15   20

ctc gcc ctg gcc ctg tgc gtg ccc ggg gcc cgg ggc cgg gct ctc gag   210

Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly Arg Ala Leu Glu

      25   30   35

tgg ttc tcg gcc gtg gta aac atc gag tac gtg gac ccg cag acc aac   258

Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp Pro Gln Thr Asn

      40   45   50

ctg acg gtg tgg agc gtc tcg gag agt ggc cgc ttc ggc gac agc tcg   306

Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe Gly Asp Ser Ser

      55   60   65

ccc aag gag ggc gcg cat ggc ctg gtg ggc gtc ccg tgg gcg ccc ggc   354

Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro Trp Ala Pro Gly

      70   75   80

gga gac ctc gag ggc tgc gcg ccc gac acg cgc ttc ttc gtg ccc gag   402

Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe Phe Val Pro Glu

85   90   95   100

```
ccc ggc ggc cga ggg gcc gcg ccc tgg gtc gcc ctg gtg gct cgt ggg      450
Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu Val Ala Arg Gly
            105                 110                 115

ggc tgc acc ttc aag gac aag gtg ctg gtg gcg gcg cgg agg aac gcc      498
Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala Arg Arg Asn Ala
            120                 125                 130

tcg gcc gtc gtc ctc tac aat gag gag cgc tac ggg aac atc acc ttg      546
Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly Asn Ile Thr Leu
            135                 140                 145

ccc atg tct cac gcg gga aca gga aat ata gtg gtc att atg att agc      594
Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val Ile Met Ile Ser
            150                 155                 160

tat cca aaa gga aga gaa att ttg gag ctg gtg caa aaa gga att cca      642
Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln Lys Gly Ile Pro
165                 170                 175                 180

gta acg atg acc ata ggg gtt ggc acc cgg cat gta cag gag ttc atc      690
Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val Gln Glu Phe Ile
            185                 190                 195

agc ggt cag tct gtg gtg ttt gtg gcc att gcc ttc atc acc atg atg      738
Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe Ile Thr Met Met
            200                 205                 210

att atc tcg tta gcc tgg cta ata ttt tac tat ata cag cgt ttc cta      786
Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile Gln Arg Phe Leu
            215                 220                 225

tat act ggc tct cag att gga agt cag agc cat aga aaa gaa act aag      834
```

Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg Lys Glu Thr Lys
        230   235   240

aaa gtt att ggc cag ctt cta ctt cat act gta aag cat gga gaa aag   882
Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys His Gly Glu Lys
245   250   255   260

gga att gat gtt gat gct gaa aat tgt gca gtg tgt att gaa aat ttc   930
Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys Ile Glu Asn Phe
                265   270   275

aaa gta aag gat att att aga att ctg cca tgc aag cat att ttt cat   978
Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys His Ile Phe His
                280   285   290

aga ata tgc att gac cca tgg ctt ttg gat cac cga aca tgt cca atg   1026
Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg Thr Cys Pro Met
                295   300   305

tgt aaa ctt gat gtc atc aaa gcc cta gga tat tgg gga gag cct ggg   1074
Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp Gly Glu Pro Gly
        310   315   320

gat gta cag gag atg cct gct cca gaa tct cct cct gga agg gat cca   1122
Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro Gly Arg Asp Pro
325   330   335   340

gct gca aat ttg agt cta gct tta cca gat gat gac gga agt gat gag   1170
Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp Gly Ser Asp Glu
                345   350   355

agc agt cca cca tca gcc tcc cct gct gaa tct gag cca cag tgt gat   1218
Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu Pro Gln Cys Asp

```
              360                 365                  370
ccc agc ttt aaa gga gat gca gga gaa aat acg gca ttg cta gaa gcc    1266
Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala Leu Leu Glu Ala
         375                 380                  385
ggc agg agt gac tct cgg cat gga gga ccc atc tcc tagcacac           1310
Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser
      390                 395                  400
gtgcccactg aagtggcacc aacagaagtt tggcttgaac taaaggacat tttatttttt  1370
ttactttagc acataatttg tatatttgaa ataatgtat attattttac ctattagatt   1430
ctgatttgat atacaaagga ctaagatatt ttcttcttga agagactttt cgattagtcc   1490
tcatatattt atctactaaa atagagtgtt taccatg                            1527
```

<210> 119

<211> 1905

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (125)...(703)

<400> 119

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gagcctaacc tagagtgctc gcagcagtct ttcagttgag cttggggact gcagctgtgg    60
ggagatttca gtgcattgcc tcccctgggt gctcttcatc ttggatttga aagttgagag   120
cagc atg ttt tgc cca ctg aaa ctc atc ctg ctg cca gtg tta ctg gat    169
     Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp
     1               5                  10                  15
```

```
tat tcc ttg ggc ctg aat gac ttg aat gtt tcc ccg cct gag cta aca       217
Tyr Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr
              20                  25                  30

gtc cat gtg ggt gat tca gct ctg atg gga tgt gtt ttc cag agc aca       265
Val His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr
              35                  40                  45

gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag       313
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu
              50                  55                  60

cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg       361
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val
              65                  70                  75

cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac aac tta       409
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu
    80                  85                  90                  95

tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag       457
Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln
             100                 105                 110

gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc       505
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe
             115                 120                 125

aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa gag ctc       553
Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Glu Leu
             130                 135                 140

atg gtc cat gtg ggt gga ttg att cag atg gga tgt gtt ttc cag agc       601
```

```
Met Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val Phe Gln Ser
         145                 150                 155

aca gaa gtg aaa cac gtg acc aag gta gaa tgg ata ttt tca gga cgg        649
Thr Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe Ser Gly Arg
160                 165                 170                 175

cgc gca aag gta aca agg agg aaa cat cac tgt gtt aga gaa ggc tct        697
Arg Ala Lys Val Thr Arg Arg Lys His His Cys Val Arg Glu Gly Ser
                 180                 185                 190

ggc tgatggtatc aggacaaagg tagaatcagg cacatgagga ggtgttgcaa           750
Gly

gagcctgggc tttggtgctt atcagaactg gaccttctcc tagcaatttc agctttctgg     810

tgggaaagat aactccaatg aagaacaaga acaagaagat gatgatgatg cttaacttt      870

tggatgccga tatgagattg tacatgagga gattgtattt cgttactacc acaaactcag     930

gatgtctgcg gagtactccc agagctgggg ccacttccag aatcgtgtga acctggtggg    990

ggacattttc cgcaatgacg gttccatcat gcttcaagga gtgagggagt cagatggagg    1050

aaactacacc tgcagtatcc acctagggaa cctggtgttc aagaaaacca ttgtgctgca    1110

tgtcagcccg gaagagcctc gaacactggt gaccccggca gccctgaggc ctctggtctt    1170

gggtggtaat cagttggtga tcattgtggg aattgtctgt gccacaatcc tgctgctccc    1230

tgttctgata ttgatcgtga agaagacctg tggaaataag agttcagtga attctacagt    1290

cttggtgaag aacacgaaga agactaatcc agagataaaa gaaaacccct gccattttga    1350

aagatgtgaa ggggagaaac acatttactc cccaataatt gtacgggagg tgatcgagga    1410

agaagaacca agtgaaaaat cagaggccac ctacatgacc atgcacccag tttggccttc    1470

tctgaggtca gatcggaaca actcacttga aaaaagtca ggtgggggaa tgccaaaaac     1530

acagcaagcc ttttgagaag aatggagagt cccttcatct cagcagcggt ggagactctc    1590

tcctgtgtgt gtcctgggcc actctaccag tgatttcaga ctcccgctct cccagctgtc    1650
```

```
ctcctgtctc attgtttggt caatacactg aagatggaga atttggagcc tggcagagag    1710

actggacagc tctggaggaa caggcctgct gaggggaggg gagcatggac ttggcctctg    1770

gagtgggaca ctggccctgg gaaccaggct gagctgagtg gcctcaaacc ccccgttgga    1830

tcagaccctc ctgtgggcag ggttcttagt ggatgagtta ctgggaagaa tcagagataa    1890

aaaccaaccc aaatc                                                     1905
```

<210> 120

<211> 998

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)...(832)

<400> 120

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gcacttgcca gccagtccgc ccgtccggag cccggctcgc tggggcagc atg gcg          55
                                                       Met Ala
                                                         1

ggg tcg ccg ctg ctc tgg ggg ccg cgg gcc ggg ggc gtc ggc ctt ttg      103
Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala Gly Gly Val Gly Leu Leu
          5                  10                  15

gtg ctg ctg ctg ctc ggc ctg ttt cgg ccg ccc ccc gcg ctc tgc gcg      151
Val Leu Leu Leu Leu Gly Leu Phe Arg Pro Pro Pro Ala Leu Cys Ala
         20                  25                  30

cgg ccg gta aag gag ccc cgc ggc cta agc gca gcg tct ccg ccc ttg      199
Arg Pro Val Lys Glu Pro Arg Gly Leu Ser Ala Ala Ser Pro Pro Leu
```

```
              35                    40                    45                    50

gct gag act ggc gct cct cgc cgc ttc cgg cgg tca gtg ccc cga ggt        247
Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg Arg Ser Val Pro Arg Gly
                        55                    60                    65

gag gcg gcg ggg gcg gtg cag gag ctg gcg cgg gcg ctg gcg cat ctg        295
Glu Ala Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu
                        70                    75                    80

ctg gag gcc gaa cgt cag gag cgg gcg cgg gcc gag gcg cag gag gct        343
Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala
                        85                    90                    95

gag gat cag cag gcg cgc gtc ctg gcg cag ctg ctg cgc gtc tgg ggc        391
Glu Asp Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Val Trp Gly
           100                   105                   110

gcc ccc cgc aac tct gat ccg gct ctg ggc ctg gac gac gac ccc gac        439
Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly Leu Asp Asp Asp Pro Asp
115                   120                   125                   130

gcg cct gca gcg cag ctc gct cgc gct ctg ctc cgc gcc cgc ctt gac        487
Ala Pro Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp
                        135                   140                   145

cct gcc gcc ctc gca gcc cag ctt gtc ccc gcg ccc gtc ccc gcc gcg        535
Pro Ala Ala Leu Ala Ala Gln Leu Val Pro Ala Pro Val Pro Ala Ala
                        150                   155                   160

gcg ctc cga ccc cgg ccc ccg gtc tac gac gac ggc ccc gcg ggc ccg        583
Ala Leu Arg Pro Arg Pro Pro Val Tyr Asp Asp Gly Pro Ala Gly Pro
           165                   170                   175
```

```
gat gct gag gag gca ggc gac gag aca ccc gac gtg gac ccc gag ctg      631
Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro Asp Val Asp Pro Glu Leu
    180             185                 190

ttg agg tac ttg ctg gga cgg att ctt gcg gga agc gcg gac tcc gag      679
Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala Gly Ser Ala Asp Ser Glu
195             200             205                 210

ggg gtg gca gcc ccg cgc cgc ctc cgc cgt gcc gcc gac cac gat gtg      727
Gly Val Ala Ala Pro Arg Arg Leu Arg Arg Ala Ala Asp His Asp Val
            215                 220             225

ggc tct gag ctg ccc cct gag ggc gtg ctg ggg gcg ctg ctg cgt gtg      775
Gly Ser Glu Leu Pro Pro Glu Gly Val Leu Gly Ala Leu Leu Arg Val
            230             235                 240

aaa cgc cta gag acc ccg gcg ccc cag gtg cct gca cgc cgc ctc ttg      823
Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg Leu Leu
            245             250                 255

cca ccc t gagcactgcc cggatcccgt gcaccctggg acccagaagt gccccgcca      880
Pro Pro
    260

tcccgccacc aggactgctc cccgccagca cgtccagagc aacttacccc ggccagccag      940
ccctctcacc cgaggatccc taccccctgg ccccacaata aacatgatct gaagcagc        998
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\<210\> 121

\<211\> 337

\<212\> PRT

\<213\> Homo sapiens

<400> 121

Met Thr Ala Gly Gly Gln Ala Glu Ala Glu Gly Ala Gly Gly Glu Pro
1   5   10   15

Gly Ala Ala Arg Leu Pro Ser Arg Val Ala Arg Leu Leu Ser Ala Leu
        20   25   30

Phe Tyr Gly Thr Cys Ser Phe Leu Ile Val Leu Val Asn Lys Ala Leu
        35   40   45

Leu Thr Thr Tyr Gly Phe Pro Ser Pro Ile Phe Leu Gly Ile Gly Gln
     50   55   60

Met Ala Ala Thr Ile Met Ile Leu Tyr Val Ser Lys Leu Asn Lys Ile
65   70   75   80

Ile His Phe Pro Asp Phe Asp Lys Lys Ile Pro Val Lys Leu Phe Pro
           85   90   95

Leu Pro Leu Leu Tyr Val Gly Asn His Ile Ser Gly Leu Ser Ser Thr
          100   105   110

Ser Lys Leu Ser Leu Pro Met Phe Thr Val Leu Arg Lys Phe Thr Ile
         115   120   125

Pro Leu Thr Leu Leu Leu Glu Thr Ile Ile Leu Gly Lys Gln Tyr Ser
    130   135   140

Leu Asn Ile Ile Leu Ser Val Phe Ala Ile Ile Leu Gly Ala Phe Ile
145   150   155   160

Ala Ala Gly Ser Asp Leu Ala Phe Asn Leu Glu Gly Tyr Ile Phe Val
          165   170   175

Phe Leu Asn Asp Ile Phe Thr Ala Ala Asn Gly Val Tyr Thr Lys Gln
          180   185   190

Lys Met Asp Pro Lys Glu Leu Gly Lys Tyr Gly Val Leu Phe Tyr Asn
            195   200   205

Ala Cys Phe Met Ile Ile Pro Thr Leu Ile Ile Ser Val Ser Thr Gly
            210   215   220

Asp Leu Gln Gln Ala Thr Glu Phe Asn Gln Trp Lys Asn Val Val Phe
225   230   235   240

Ile Leu Gln Phe Leu Leu Ser Cys Phe Leu Gly Phe Leu Leu Met Tyr
                245   250   255

Ser Thr Val Leu Cys Ser Tyr Tyr Asn Ser Ala Leu Thr Thr Ala Val
                260   265   270

Val Gly Ala Ile Lys Asn Val Ser Val Ala Tyr Ile Gly Ile Leu Ile
                275   280   285

Gly Gly Asp Tyr Ile Phe Ser Leu Leu Asn Phe Val Gly Leu Asn Ile
            290   295   300

Cys Met Ala Gly Gly Leu Arg Tyr Ser Phe Leu Thr Leu Ser Ser Gln
305   310   315   320

Leu Lys Pro Lys Pro Val Gly Glu Glu Asn Ile Cys Leu Asp Leu Lys
                325   330   335

Ser

<210> 122

<211> 236

<212> PRT

<213> Homo sapiens

<400> 122

Met Ala Glu Ala Glu Glu Ser Pro Gly Asp Pro Gly Thr Ala Ser Pro
1   5   10   15

Arg Pro Leu Phe Ala Gly Leu Ser Asp Ile Ser Ile Ser Gln Asp Ile
                20   25   30

Pro Val Glu Gly Glu Ile Thr Ile Pro Met Arg Ser Arg Ile Arg Glu
                35   40   45

Phe Asp Ser Ser Thr Leu Asn Glu Ser Val Arg Asn Thr Ile Met Arg
        50   55   60

Asp Leu Lys Ala Val Gly Lys Lys Phe Met His Val Leu Tyr Pro Arg
65   70   75   80

Lys Ser Asn Thr Leu Leu Arg Asp Trp Asp Leu Trp Gly Pro Leu Ile
                85   90   95

Leu Cys Val Thr Leu Ala Leu Met Leu Gln Arg Asp Ser Ala Asp Ser
                100   105   110

Glu Lys Asp Gly Gly Pro Gln Phe Ala Glu Val Phe Val Ile Val Trp
        115   120   125

Phe Gly Ala Val Thr Ile Thr Leu Asn Ser Lys Leu Leu Gly Gly Asn
        130   135   140

Ile Ser Phe Phe Gln Ser Leu Cys Val Leu Gly Tyr Cys Ile Leu Pro
145   150   155   160

Leu Thr Val Ala Met Leu Ile Cys Arg Leu Val Leu Leu Ala Asp Pro
                165   170   175

Gly Pro Val Asn Phe Met Val Arg Leu Phe Val Val Ile Val Met Phe
                180   185   190

Ala Trp Ser Ile Val Ala Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro

        195   200   205

Pro Asn Arg Arg Ala Leu Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe

        210   215   220

Val Ile Ser Trp Met Ile Leu Thr Phe Thr Pro Gln

225   230   235

<210> 123

<211> 560

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Ala Pro Ala Glu Ser Leu Arg Arg Arg Lys Thr Gly Tyr Ser

 1   5   10   15

Asp Pro Glu Pro Glu Ser Pro Pro Ala Pro Gly Arg Gly Pro Ala Gly

                20   25   30

Ser Pro Ala His Leu His Thr Gly Thr Phe Trp Leu Thr Arg Ile Val

                35   40   45

Leu Leu Lys Ala Leu Ala Phe Val Tyr Phe Val Ala Phe Leu Val Ala

        50   55   60

Phe His Gln Asn Lys Gln Leu Ile Gly Asp Arg Gly Leu Leu Pro Cys

65   70   75   80

Arg Val Phe Leu Lys Asn Phe Gln Gln Tyr Phe Gln Asp Arg Thr Ser

                85   90   95

Trp Glu Val Phe Ser Tyr Met Pro Thr Ile Leu Trp Leu Met Asp Trp

                    100   105   110
Ser Asp Met Asn Ser Asn Leu Asp Leu Leu Ala Leu Leu Gly Leu Gly

                    115   120   125
Ile Ser Ser Phe Val Leu Ile Thr Gly Cys Ala Asn Met Leu Leu Met

        130   135   140
Ala Ala Leu Trp Gly Leu Tyr Met Ser Leu Val Asn Val Gly His Val

145   150   155   160
Trp Tyr Ser Phe Gly Trp Glu Ser Gln Leu Leu Glu Thr Gly Phe Leu

                    165   170   175
Gly Ile Phe Leu Cys Pro Leu Trp Thr Leu Ser Arg Leu Pro Gln His

                    180   185   190
Thr Pro Thr Ser Arg Ile Val Leu Trp Gly Phe Arg Trp Leu Ile Phe

            195   200   205
Arg Ile Met Leu Gly Ala Gly Leu Ile Lys Ile Arg Gly Asp Arg Cys

        210   215   220
Trp Arg Asp Leu Thr Cys Met Asp Phe His Tyr Glu Thr Gln Pro Met

225   230   235   240
Pro Asn Pro Val Ala Tyr Tyr Leu His His Ser Pro Trp Trp Phe His

                    245   250   255
Arg Phe Glu Thr Leu Ser Asn His Phe Ile Glu Leu Leu Val Pro Phe

            260   265   270
Phe Leu Phe Leu Gly Arg Arg Ala Cys Ile Ile His Gly Val Leu Gln

            275   280   285
Ile Leu Phe Gln Ala Val Leu Ile Val Ser Gly Asn Leu Ser Phe Leu

    290   295   300

Asn Trp Leu Thr Met Val Pro Ser Leu Ala Cys Phe Asp Asp Ala Thr
305   310   315   320

Leu Gly Phe Leu Phe Pro Ser Gly Pro Gly Ser Leu Lys Asp Arg Val
                325   330   335

Leu Gln Met Gln Arg Asp Ile Arg Gly Ala Arg Pro Glu Pro Arg Phe
                340   345   350

Gly Ser Val Val Arg Arg Ala Ala Asn Val Ser Leu Gly Val Leu Leu
                355   360   365

Ala Trp Leu Ser Val Pro Val Val Leu Asn Leu Leu Ser Ser Arg Gln
        370   375   380

Val Met Asn Thr His Phe Asn Ser Leu His Ile Val Asn Thr Tyr Gly
385   390   395   400

Ala Phe Gly Ser Ile Thr Lys Glu Arg Ala Glu Val Ile Leu Gln Gly
                405   410   415

Thr Ala Ser Ser Asn Ala Ser Ala Pro Asp Ala Met Trp Glu Asp Tyr
                420   425   430

Glu Phe Lys Cys Lys Pro Gly Asp Pro Ser Arg Arg Pro Cys Leu Ile
                435   440   445

Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu Met Trp Phe Ala Ala Phe
        450   455   460

Gln Thr Tyr Glu His Asn Asp Trp Ile Ile His Leu Ala Gly Lys Leu
465   470   475   480

Leu Ala Ser Asp Ala Glu Ala Leu Ser Leu Leu Ala His Asn Pro Phe
                485   490   495

Ala Gly Arg Pro Pro Pro Arg Trp Val Arg Gly Glu His Tyr Arg Tyr

        500   505   510

Lys Phe Ser Arg Pro Gly Gly Arg His Ala Ala Glu Gly Lys Trp Trp

        515   520   525

Val Arg Lys Arg Ile Gly Ala Tyr Phe Pro Pro Leu Ser Leu Glu Glu

        530   535   540

Leu Arg Pro Tyr Phe Arg Asp Arg Gly Trp Pro Leu Pro Gly Pro Leu

545   550   555   560

<210> 124

<211> 406

<212> PRT

<213> Homo sapiens

<400> 124

Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn

1   5   10   15

Lys Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu

                20   25   30

Lys Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg

                35   40   45

Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile

        50   55   60

Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val

65   70   75   80

Ser Phe Leu Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu

                85   90   95

Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu
        100   105   110

Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly
        115   120   125

Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser
        130   135   140

Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro
145   150   155   160

Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly
            165   170   175

Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys
        180   185   190

Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met
        195   200   205

Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr
        210   215   220

Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe
225   230   235   240

Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly
            245   250   255

Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp
        260   265   270

Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe
        275   280   285

Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln

```
          290                  295                  300
Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met
305                  310                  315                  320
Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys
                     325                  330                  335
Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys
                     340                  345                  350
Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe
                     355                  360                  365
Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile
                     370                  375                  380
Asn Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn
385                  390                  395                  400
Ser Glu Glu Lys Thr Lys
                     405
```

<210> 125

<211> 453

<212> PRT

<213> Homo sapiens

<400> 125

```
Met Gly Val Leu Gly Arg Val Leu Leu Trp Leu Gln Leu Cys Ala Leu
 1               5                   10                  15
Thr Gln Ala Val Ser Lys Leu Trp Val Pro Asn Thr Asp Phe Asp Val
          20                  25                  30
```

Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly Gly Ala Val

            35   40   45

Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val Gln Glu Gly His

            50   55   60

Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly Glu Leu Val Leu Ala

65   70   75   80

Ser Gly Ala Gly Phe Gly Val Ser Asp Val Gly Ser His Leu Asp Cys

                 85   90   95

Gly Ala Gly Glu Pro Ala Val Phe Arg Asp Ser Asp Arg Phe Ser Trp

                 100   105   110

His Asp Pro His Leu Trp Arg Ser Gly Asp Glu Ala Pro Gly Leu Phe

            115   120   125

Phe Val Asp Ala Glu Arg Val Pro Cys Arg His Asp Asp Val Phe Phe

            130   135   140

Pro Pro Ser Ala Ser Phe Arg Val Gly Leu Gly Pro Gly Ala Ser Pro

145   150   155   160

Val Arg Val Arg Ser Ile Ser Ala Leu Gly Arg Thr Phe Thr Arg Asp

                 165   170   175

Glu Asp Leu Ala Val Phe Leu Ala Ser Arg Ala Gly Arg Leu Arg Phe

            180   185   190

His Gly Pro Gly Ala Leu Ser Val Gly Pro Glu Asp Cys Ala Asp Pro

            195   200   205

Ser Gly Cys Val Cys Gly Asn Ala Glu Ala Gln Pro Trp Ile Cys Ala

            210   215   220

Ala Leu Leu Gln Pro Leu Gly Gly Arg Cys Pro Gln Ala Ala Cys His

| 225 | | 230 | | 235 | | 240 |

Ser Ala Leu Arg Pro Gln Gly Gln Cys Cys Asp Leu Cys Gly Ala Val

| | 245 | | 250 | | 255 |

Val Leu Leu Thr His Gly Pro Ala Phe Asp Leu Glu Arg Tyr Arg Ala

| | 260 | | 265 | | 270 |

Arg Ile Leu Asp Thr Phe Leu Gly Leu Pro Gln Tyr His Gly Leu Gln

| | 275 | | 280 | | 285 |

Val Ala Val Ser Lys Val Pro Arg Ser Ser Arg Leu Arg Glu Ala Asp

| 290 | | 295 | | 300 |

Thr Glu Ile Gln Val Val Leu Val Glu Asn Gly Pro Glu Thr Gly Gly

| 305 | | 310 | | 315 | | 320 |

Ala Gly Arg Leu Ala Arg Ala Leu Leu Ala Asp Val Ala Glu Asn Gly

| | 325 | | 330 | | 335 |

Glu Ala Leu Gly Val Leu Glu Ala Thr Met Arg Glu Ser Gly Ala His

| | 340 | | 345 | | 350 |

Val Trp Gly Ser Ser Ala Ala Gly Leu Ala Gly Gly Val Ala Ala Ala

| | 355 | | 360 | | 365 |

Val Leu Leu Ala Leu Leu Val Leu Leu Val Ala Pro Pro Leu Leu Arg

| 370 | | 375 | | 380 |

Arg Ala Gly Arg Leu Arg Trp Arg Arg His Glu Ala Ala Ala Pro Ala

| 385 | | 390 | | 395 | | 400 |

Gly Ala Pro Leu Gly Phe Arg Asn Pro Val Phe Asp Val Thr Ala Ser

| | 405 | | 410 | | 415 |

Glu Glu Leu Pro Leu Pro Arg Arg Leu Ser Leu Val Pro Lys Ala Ala

| | 420 | | 425 | | 430 |

Ala Asp Ser Thr Ser His Ser Tyr Phe Val Asn Pro Leu Phe Ala Gly

      435   440   445

Ala Glu Ala Glu Ala

     450

<210> 126

<211> 59

<212> PRT

<213> Homo sapiens

<400> 126

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu

  1   5   10   15

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala

        20   25   30

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Cys Ala Cys Leu

     35   40   45

Gly Val Tyr Ala Arg Lys Arg Asn Gly Gln Met

    50   55

<210> 127

<211> 210

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Leu Pro Gln Met Cys Asp Gly Ser His Leu Ala Ser Thr Leu

1				5					10					15
Arg	Tyr	Cys	Met	Thr	Val	Ser	Gly	Thr	Val	Val	Leu	Val	Ala	Gly	Thr

```
              20                    25                    30
Leu Cys Phe Ala Trp Trp Ser Glu Gly Asp Ala Thr Ala Gln Pro Gly

        35                    40                    45
Gln Leu Ala Pro Pro Thr Glu Tyr Pro Val Pro Glu Gly Pro Ser Pro

      50                    55                    60
Leu Leu Arg Ser Val Ser Phe Val Cys Cys Gly Ala Gly Gly Leu Leu

65                    70                    75                    80
Leu Leu Ile Gly Leu Leu Trp Ser Val Lys Ala Ser Ile Pro Gly Pro

                    85                    90                    95
Pro Arg Trp Asp Pro Tyr His Leu Ser Arg Asp Leu Tyr Tyr Leu Thr

                  100                   105                   110
Val Glu Ser Ser Glu Lys Glu Ser Cys Arg Thr Pro Lys Val Val Asp

                115                   120                   125
Ile Pro Thr Tyr Glu Glu Ala Val Ser Phe Pro Val Ala Glu Gly Pro

              130                   135                   140
Pro Thr Pro Pro Ala Tyr Pro Thr Glu Glu Ala Leu Glu Pro Ser Gly

145                   150                   155                   160
Ser Arg Asp Ala Leu Leu Ser Thr Gln Pro Ala Trp Pro Pro Pro Ser

                  165                   170                   175
Tyr Glu Ser Ile Ser Leu Ala Leu Asp Ala Val Ser Ala Glu Thr Thr

                180                   185                   190
Pro Ser Ala Thr Arg Ser Cys Ser Gly Leu Val Gln Thr Ala Arg Gly

              195                   200                   205
```

Gly Ser

   210

<210> 128

<211> 165

<212> PRT

<213> Homo sapiens

<400> 128

Met Asp Ser Ser Arg Ala Arg Gln Gln Leu Arg Arg Arg Phe Leu Leu
 1   5   10   15

Leu Pro Asp Ala Glu Ala Gln Leu Asp Arg Glu Gly Asp Ala Gly Pro
                20   25   30

Glu Thr Ser Thr Ala Val Glu Lys Lys Glu Lys Pro Leu Pro Arg Leu
                35   40   45

Asn Ile His Ser Gly Phe Trp Ile Leu Ala Ser Ile Val Val Thr Tyr
            50   55   60

Tyr Val Asp Phe Phe Lys Thr Leu Lys Glu Asn Phe His Thr Ser Ser
65   70   75   80

Trp Phe Leu Cys Gly Ser Ala Leu Leu Leu Val Ser Leu Ser Ile Ala
                85   90   95

Phe Tyr Cys Ile Val Tyr Leu Glu Trp Tyr Cys Gly Ile Gly Glu Tyr
                100   105   110

Asp Val Lys Tyr Pro Ala Leu Ile Pro Ile Thr Thr Ala Ser Phe Ile
            115   120   125

Ala Ala Gly Ile Cys Phe Asn Ile Ala Leu Trp His Val Trp Ser Phe

            130   135   140

Phe Thr Pro Leu Leu Leu Phe Thr Gln Phe Met Gly Val Val Met Phe

145   150   155   160

Ile Thr Leu Leu Gly

                165

<210> 129

<211> 162

<212> PRT

<213> Homo sapiens

<400> 129

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu

  1   5   10   15

Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln

                20   25   30

Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala

                35   40   45

Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe

                50   55   60

Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly

65   70   75   80

Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His

                85   90   95

Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp

                100   105   110

Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val

            115   120   125

Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro

            130   135   140

His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val

145   150   155   160

Arg Arg

<210> 130

<211> 221

<212> PRT

<213> Homo sapiens

<400> 130

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly

 1   5   10   15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu

            20   25   30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

            35   40   45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro

            50   55   60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu

65   70   75   80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu

                 85   90   95

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile
                100   105   110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe
                115   120   125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala
            130   135   140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp
145   150   155   160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly
                165   170   175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe
                180   185   190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr
                195   200   205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr
210   215   220

<210> 131

<211> 1011

<212> DNA

<213> Homo sapiens

<400> 131

atgacggccg gcggccaggc cgaggccgag ggcgctggcg gggagcccgg cgcggcgcgg   60

ctgccctcgc gggtggcccg gctgctgtcg gcgctcttct acgggacctg ctccttcctc   120

atcgtgcttg tcaacaaggc gctgctgacc acctacggtt tcccgtcacc aattttcctt   180

```
ggaattggac agatggcagc caccataatg atactatatg tgtccaagct aaacaaaatc     240

attcacttcc ctgattttga taagaaaatt cctgtaaagc tgtttcctct gcctctcctc     300

tacgttggaa accacataag tggattatca agcacaagta aattaagcct accgatgttc     360

accgtgctca ggaaattcac cattccactt accttacttc tggaaaccat catacttggg     420

aagcagtatt cactcaacat catcctcagt gtctttgcca ttattctcgg ggctttcata     480

gcagctgggt ctgaccttgc ttttaactta gaaggctata tttttgtatt cctgaatgat     540

atcttcacag cagcaaatgg agtttatacc aaacagaaaa tggacccaaa ggagctaggg     600

aaatacggag tacttttcta caatgcctgc ttcatgatta tcccaactct tattattagt     660

gtctccactg gagacctgca acaggctact gaattcaacc aatggaagaa tgttgtgttt     720

atcctacagt ttcttctttc ctgttttttg gggtttctgc tgatgtactc cacggttctg     780

tgcagctatt acaattcagc cctgacgaca gcagtggttg gagccatcaa gaatgtatcc     840

gttgcctaca ttgggatatt aatcggtgga gactacattt tctctttgtt aaactttgta     900

gggttaaata tttgcatggc aggggggcttg agatattcct ttttaacact gagcagccag     960

ttaaaaccta aacctgtggg tgaagaaaac atctgtttgg atttgaagag c              1011
```

<210> 132

<211> 708

<212> DNA

<213> Homo sapiens

<400> 132

```
atggcggaag cggaggagtc tccaggagac ccggggacag catcgcccag gcccctgttt      60

gcaggccttt cagatatatc catctcacaa gacatccccg tagaaggaga aatcaccatt     120

cctatgagat ctcgcatccg ggagtttgac agctccacat taaatgaatc tgttcgcaat     180

accatcatgc gtgatctaaa agctgttggg aaaaaattca tgcatgtttt gtacccaagg     240

aaaagtaata ctcttttgag agattgggat ttgtggggcc ctttgatcct ttgtgtgaca     300
```

```
ctcgcattaa tgctgcaaag agactctgca gatagtgaaa aagatggagg gccccaattt    360

gcagaggtgt ttgtcattgt ctggtttggt gcagttacca tcaccctcaa ctcaaaactt    420

cttggaggga acatatcttt ttttcagagc ctctgtgtgc tgggttactg tatacttccc    480

ttgacagtag caatgctgat ttgccggctg gtacttttgg ctgatccagg acctgtaaac    540

ttcatggttc ggctttttgt ggtgattgtg atgtttgcct ggtctatagt tgcctccaca    600

gctttccttg ctgatagcca gcctccaaac cgcagagccc tagctgttta tcctgttttc    660

ctgttttact ttgtcatcag ttggatgatt ctcacccttta ctcctcag                708
```

<210> 133

<211> 1680

<212> DNA

<213> Homo sapiens

<400> 133

```
atggcggcgc ccgcggagtc gctgaggagg cggaagactg ggtactcgga tccggagcct    60

gagtcgccgc ccgcgccggg gcgtggcccc gcaggctctc cggcccatct ccacacgggc    120

accttctggc tgacccggat cgtgctcctg aaggccctag ccttcgtgta cttcgtggca    180

ttcctggtgg ctttccatca gaacaagcag ctcatcggtg acaggggggct gcttccctgc    240

agagtgttcc tgaagaactt ccagcagtac ttccaggaca ggacgagctg ggaagtcttc    300

agctacatgc ccaccatcct ctggctgatg gactggtcag acatgaactc caacctggac    360

ttgctggctc ttctcggact gggcatctcg tctttcgtac tgatcacggg ctgcgccaac    420

atgcttctca tggctgccct gtggggcctc tacatgtccc tggttaatgt gggccatgtc    480

tggtactctt tcggatggga gtcccagctt ctggagacgg ggttcctggg gatcttcctg    540

tgccctctgt ggacgctgtc aaggctgccc cagcataccc ccacatcccg gattgtcctg    600

tggggcttcc ggtggctgat cttcaggatc atgcttggag caggcctgat caagatccgg    660

ggggaccggt gctggcgaga cctcacctgc atggacttcc actatgagac ccagccgatg    720
```

```
cccaatcctg tggcatacta cctgcaccac tcaccctggt ggttccatcg cttcgagacg   780

ctcagcaacc acttcatcga gctcctggtg cccttcttcc tcttcctcgg ccggcgggcg   840

tgcatcatcc acggggtgct gcagatcctg ttccaggccg tcctcatcgt cagcgggaac   900

ctcagcttcc tgaactggct gactatggtg cccagcctgg cctgctttga tgacgccacc   960

ctgggattct tgttcccctc tgggccaggc agcctgaagg accgagttct gcagatgcag  1020

agggacatcc gaggggcccg gcccgagccc agattcggct ccgtggtgcg gcgtgcagcc  1080

aacgtctcgc tgggcgtcct gctggcctgg ctcagcgtgc ccgtggtcct caacttgctg  1140

agctccaggc aggtcatgaa cacccacttc aactctcttc acatcgtcaa cacttacggg  1200

gccttcggaa gcatcaccaa ggagcgggcg gaggtgatcc tgcagggcac agccagctcc  1260

aacgccagcg cccccgatgc catgtgggag gactacgagt tcaagtgcaa gccaggtgac  1320

cccagcagac ggccctgcct catctccccg taccactacc gcctggactg gctgatgtgg  1380

ttcgcggcct tccagaccta cgagcacaac gactggatca tccacctggc tggcaagctc  1440

ctggccagcg acgccgaggc cttgtccctg ctggcacaca accccttcgc gggcaggccc  1500

ccgcccaggt gggtccgagg agagcactac aggtacaagt tcagccgtcc tggggggcagg  1560

cacgccgccg agggcaagtg gtgggtgcgg aagaggatcg gagcctactt ccctccgctc  1620

agcctggagg agctgaggcc ctacttcagg gaccgtgggt ggcctctgcc cgggcccctc  1680
```

<210> 134

<211> 1218

<212> DNA

<213> Homo sapiens

<400> 134

```
atggcagaga atggaaaaaa ttgtgaccag agacgtgtag caatgaacaa ggaacatcat    60

aatggaaatt tcacagaccc ctcttcagtg aatgaaaaga agagagggga gcgggaagaa   120

aggcagaata ttgtcctgtg gagacagccg ctcattacct tgcagtattt ttctctggaa   180
```

```
atccttgtaa tcttgaagga atggacctca aaattatggc atcgtcaaag cattgtggtg    240

tcttttttac tgctgcttgc tgtgcttata gctacgtatt atgttgaagg agtgcatcaa    300

cagtatgtgc aacgtataga gaaacagttt cttttgtatg cctactggat aggcttagga    360

attttgtctt ctgttgggct tggaacaggg ctgcacacct ttctgcttta tctgggtcca    420

catatagcct cagttacatt agctgcttat gaatgcaatt cagttaattt tcccgaacca    480

ccctatcctg atcagattat ttgtccagat gaagagggca ctgaaggaac catttctttg    540

tggagtatca tctcaaaagt taggattgaa gcctgcatgt ggggtatcgg tacagcaatc    600

ggagagctgc ctccatattt catggccaga gcagctcgcc tctcaggtgc tgaaccagat    660

gatgaagagt atcaggaatt tgaagagatg ctggaacatg cagagtctgc acaagacttt    720

gcctcccggg ccaaactggc agttcaaaaa ctagtacaga aagttggatt ttttggaatt    780

ttggcctgtg cttcaattcc aaatccttta tttgatctgg ctggaataac gtgtggacac    840

tttctggtac cttttggac cttctttggt gcaaccctaa ttggaaaagc aataataaaa    900

atgcatatcc agaaaatttt tgttataata acattcagca agcacatagt ggagcaaatg    960

gtggctttca ttggtgctgt ccccggcata ggtccatctc tgcagaagcc atttcaggag   1020

tacctggagg ctcaacggca gaagcttcac cacaaaagcg aaatgggcac accacaggga   1080

gaaaactggt tgtcctggat gtttgaaaag ttggtcgttg tcatggtgtg ttacttcatc   1140

ctatctatca ttaactccat ggcacaaagt tatgccaaac gaatccagca gcggttgaac   1200

tcagaggaga aaactaaa                                                  1218
```

<210> 135

<211> 1359

<212> DNA

<213> Homo sapiens

<400> 135

```
atgggcgtcc tgggccgggt cctgctgtgg ctgcagctct gcgcactgac ccaggcggtc     60
```

```
tccaaactct gggtccccaa cacggacttc gacgtcgcag ccaactggag ccagaaccgg    120

accccgtgcg ccggcggcgc cgttgagttc ccggcggaca agatggtgtc agtcctggtg    180

caagaaggtc acgccgtctc agacatgctc ctgccgctgg atggggaact cgtcctggct    240

tcaggagccg gattcggcgt ctcagacgtg ggctcgcacc tggactgtgg cgcgggcgaa    300

cctgccgtct tccgcgactc tgaccgcttc tcctggcatg acccgcacct gtggcgctct    360

ggggacgagg cacctggcct cttcttcgtg gacgccgagc gcgtgccctg ccgccacgac    420

gacgtcttct ttccgcctag tgcctccttc cgcgtggggc tcggccctgg cgctagcccc    480

gtgcgtgtcc gcagcatctc ggctctgggc cggacgttca cgcgcgacga ggacctggct    540

gttttcctgg cgtcccgcgc gggccgccta cgcttccacg ggccgggcgc gctgagcgtg    600

ggccccgagg actgcgcgga cccgtcgggc tgcgtctgcg gcaacgcgga ggcgcagccg    660

tggatctgcg cggccctgct ccagcccctg ggcggccgct gcccccaggc cgcctgccac    720

agcgccctcc ggccccaggg gcagtgctgt gacctctgtg gagccgttgt gttgctgacc    780

cacggccccg catttgacct ggagcggtac cgggcgcgga tactggacac cttcctgggt    840

ctgcctcagt accacgggct gcaggtggcc gtgtccaagg tgccacgctc gtcccggctc    900

cgtgaggccg atacggagat ccaggtggtg ctggtggaga tggggcccga gacaggcgga    960

gcggggcggc tggcccgggc cctcctggcg gacgtcgccg agaacggcga ggccctcggc   1020

gtcctggagg cgaccatgcg ggagtcgggc gcacacgtct ggggcagctc cgcggctggg   1080

ctggcgggcg gcgtggcggc tgccgtgctg ctggcgctgc tggtcctgct ggtggcgccg   1140

ccgctgctgc ccgcgcgggg gaggctcagg tggaggaggc acgaggcggc ggccccggct   1200

ggagcgcccc tcggcttccg caacccggtg ttcgacgtga cggcctccga ggagctgccc   1260

ctgccgcggc ggctcagcct ggttccgaag gcggccgcag acagcaccag ccacagttac   1320

ttcgtcaacc ctctgttcgc cggggccgag gccgaggcc                         1359
```

<210> 136

<211> 177

<212> DNA

<213> Homo sapiens

<400> 136

```
atgacctcag tttcaacaca gttgtcctta gtcctcatgt cactgctttt ggtgctgcct        60

gttgtggaag cagtagaagc cggtgatgca atcgccettt tgttaggtgt ggttctcagc       120

attacaggca tttgtgcctg cttgggggta tatgcacgaa aaagaaatgg acagatg          177

atgacctcag tttcaacaca gttgtcctta gtcctcatgt cactgctttt ggtgctgcct        60

gttgtggaag cagtagaagc cggtgatgca atcgccettt tgttaggtgt ggttctcagc       120

attacaggca tttgtgcctg cttgggggta tatgcacgaa aaagaaatgg acagatg          177
```

<210> 137

<211> 630

<212> DNA

<213> Homo sapiens

<400> 137

```
atggccctgc cccagatgtg tgacgggagc cacttggcct ccaccctccg ctattgcatg        60

acagtcagcg gcacagtggt tctggtggcc gggacgctct gcttcgcttg gtggagcgaa       120

ggggatgcaa ccgcccagcc tggccagctg gccccaccca cggagtatcc ggtgcctgag       180

ggccccagcc ccctgctcag gtccgtcagc ttcgtctgct gcggtgcagg tggcctgctg       240

ctgctcattg gcctgctgtg gtccgtcaag gccagcatcc cagggccacc tcgatgggac       300

ccctatcacc tctccagaga cctgtactac ctcactgtgg agtcctcaga gaaggagagc       360

tgcaggaccc ccaaagtggt tgacatcccc acttacgagg aagccgtgag cttcccagtg       420

gccgaggggc ccccaacacc acctgcatac cctacggagg aagccctgga gccaagtgga       480

tcgagggatg ccctgctcag cacccagccc gcctggcctc cacccagcta tgagagcatc       540

agccttgctc ttgatgccgt ttctgcagag acgacaccga gtgccacacg ctcctgctca       600
```

ggcctggttc agactgcacg gggaggaagt   630

<210> 138

<211> 495

<212> DNA

<213> Homo sapiens

<400> 138

atggactcct cgcgggcccg acagcagctc cggcggcgat tcctcctcct gccggacgcc   60

gaggcccagc tggaccgcga gggtgacgcc gggccggaaa cctccacagc tgttgagaaa   120

aaggagaaac ctcttccaag acttaatatc cattctggat tctggatttt ggcatccatt   180

gttgtgacct attatgttga cttctttaaa acccttaaag aaaacttcca cactagcagc   240

tggtttctct gtggcagtgc cttgttgctt gtcagtttat caattgcatt ttactgcata   300

gtctacctgg aatggtattg tggaattgga gaatatgatg tcaagtatcc agccttgata   360

cccattacca ctgcctcctt tattgcagca ggaatttgct tcaacattgc tttatggcat   420

gtgtggtcgt ttttcactcc attgttgttg tttacccagt ttatgggggt tgtcatgttt   480

atcacactcc ttgga   495

<210> 139

<211> 486

<212> DNA

<213> Homo sapiens

<400> 139

atgctccaga ccagtaacta cagcctggtg ctctctctgc agttcctgct gctgtcctat   60

gacctctttg tcaattcctt ctcagaactg ctccaaaaga ctcctgtcat ccagcttgtg   120

ctcttcatca tccaggatat tgcagtcctc ttcaacatca tcatcatttt cctcatgttc   180

```
ttcaacacct tcgtcttcca ggctggcctg gtcaacctcc tattccataa gttcaaaggg    240

accatcatcc tgacagctgt gtactttgcc ctcagcatct cccttcatgt ctgggtcatg    300

aacttacgct ggaaaaactc caacagcttc atatggacag atggacttca aatgctgttt    360

gtattccaga gactagcagc agtgttgtac tgctacttct ataaacggac agccgtaaga    420

ctaggcgatc ctcacttcta ccaggactct ttgtggctgc gcaaggagtt catgcaagtt    480

cgaagg                                                               486
```

<210> 140

<211> 663

<212> DNA

<213> Homo sapiens

<400> 140

```
atggcgttgg cgttggcggc gctggcggcg gtcgagccgg cctgcggcag ccggtaccag    60

cagttgcaga atgaagaaga gtctggagaa cctgaacagg ctgcaggtga tgctcctcca    120

ccttacagca gcatttctgc agagagcgca gcatattttg actacaagga tgagtctggg    180

tttccaaagc ccccatctta caatgtagct acaacactgc ccagttatga tgaagcggag    240

aggaccaagg ctgaagctac tatccctttg gttcctggga gagatgagga ttttgtgggt    300

cgggatgatt ttgatgatgc tgaccagctg aggataggaa atgatgggat tttcatgtta    360

acttttttca tggcattcct ctttaactgg attgggtttt tcctgtcttt ttgcctgacc    420

acttcagctg caggaaggta tggggccatt tcaggatttg gtctctctct aattaaatgg    480

atcctgattg tcaggttttc cacctatttc cctggatatt ttgatggtca gtactggctc    540

tggtgggtgt tccttgtttt aggctttctc ctgtttctca gaggatttat caattatgca    600

aaagttcgga agatgccaga aactttctca aatctcccca ggaccagagt tctctttatt    660

tat                                                                  663
```

<210> 141

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78)...(1091)

<400> 141

ctcttccccg	gcccggccgg	gcgggaccag	tgcgcagccg	gggctggcgg	gcggcggggt	60

ccgcggggcc	gcaggag	atg	acg	gcc	ggc	ggc	cag	gcc	gag	gcc	gag	ggc	110

                 Met Thr Ala Gly Gly Gln Ala Glu Ala Glu Gly

                1   5   10

gct ggc ggg gag ccc ggc gcg gcg cgg ctg ccc tcg cgg gtg gcc cgg   158

Ala Gly Gly Glu Pro Gly Ala Ala Arg Leu Pro Ser Arg Val Ala Arg

          15   20   25

ctg ctg tcg gcg ctc ttc tac ggg acc tgc tcc ttc ctc atc gtg ctt   206

Leu Leu Ser Ala Leu Phe Tyr Gly Thr Cys Ser Phe Leu Ile Val Leu

         30   35   40

gtc aac aag gcg ctg ctg acc acc tac ggt ttc ccg tca cca att ttc   254

Val Asn Lys Ala Leu Leu Thr Thr Tyr Gly Phe Pro Ser Pro Ile Phe

        45   50   55

ctt gga att gga cag atg gca gcc acc ata atg ata cta tat gtg tcc   302

Leu Gly Ile Gly Gln Met Ala Ala Thr Ile Met Ile Leu Tyr Val Ser

60   65   70   75

aag cta aac aaa atc att cac ttc cct gat ttt gat aag aaa att cct   350

Lys Leu Asn Lys Ile Ile His Phe Pro Asp Phe Asp Lys Lys Ile Pro

                   80   85   90

gta aag ctg ttt cct ctg cct ctc ctc tac gtt gga aac cac ata agt   398

Val Lys Leu Phe Pro Leu Pro Leu Leu Tyr Val Gly Asn His Ile Ser

                   95   100   105

gga tta tca agc aca agt aaa tta agc cta ccg atg ttc acc gtg ctc   446

Gly Leu Ser Ser Thr Ser Lys Leu Ser Leu Pro Met Phe Thr Val Leu

                 110   115   120

agg aaa ttc acc att cca ctt acc tta ctt ctg gaa acc atc ata ctt   494

Arg Lys Phe Thr Ile Pro Leu Thr Leu Leu Leu Glu Thr Ile Ile Leu

                 125   130   135

ggg aag cag tat tca ctc aac atc atc ctc agt gtc ttt gcc att att   542

Gly Lys Gln Tyr Ser Leu Asn Ile Ile Leu Ser Val Phe Ala Ile Ile

140   145   150   155

ctc ggg gct ttc ata gca gct ggg tct gac ctt gct ttt aac tta gaa   590

Leu Gly Ala Phe Ile Ala Ala Gly Ser Asp Leu Ala Phe Asn Leu Glu

                 160   165   170

ggc tat att ttt gta ttc ctg aat gat atc ttc aca gca gca aat gga   638

Gly Tyr Ile Phe Val Phe Leu Asn Asp Ile Phe Thr Ala Ala Asn Gly

                 175   180   185

gtt tat acc aaa cag aaa atg gac cca aag gag cta ggg aaa tac gga   686

Val Tyr Thr Lys Gln Lys Met Asp Pro Lys Glu Leu Gly Lys Tyr Gly

               190   195   200

gta ctt ttc tac aat gcc tgc ttc atg att atc cca act ctt att att   734

Val Leu Phe Tyr Asn Ala Cys Phe Met Ile Ile Pro Thr Leu Ile Ile

```
             205                    210                    215

agt gtc tcc act gga gac ctg caa cag gct act gaa ttc aac caa tgg        782
Ser Val Ser Thr Gly Asp Leu Gln Gln Ala Thr Glu Phe Asn Gln Trp
220                    225                    230                    235
aag aat gtt gtg ttt atc cta cag ttt ctt ctt tcc tgt ttt ttg ggg        830
Lys Asn Val Val Phe Ile Leu Gln Phe Leu Leu Ser Cys Phe Leu Gly
                     240                    245                    250
ttt ctg ctg atg tac tcc acg gtt ctg tgc agc tat tac aat tca gcc        878
Phe Leu Leu Met Tyr Ser Thr Val Leu Cys Ser Tyr Tyr Asn Ser Ala
                     255                    260                    265
ctg acg aca gca gtg gtt gga gcc atc aag aat gta tcc gtt gcc tac        926
Leu Thr Thr Ala Val Val Gly Ala Ile Lys Asn Val Ser Val Ala Tyr
             270                    275                    280
att ggg ata tta atc ggt gga gac tac att ttc tct ttg tta aac ttt        974
Ile Gly Ile Leu Ile Gly Gly Asp Tyr Ile Phe Ser Leu Leu Asn Phe
             285                    290                    295
gta ggg tta aat att tgc atg gca ggg ggc ttg aga tat tcc ttt tta       1022
Val Gly Leu Asn Ile Cys Met Ala Gly Gly Leu Arg Tyr Ser Phe Leu
300                    305                    310                    315
aca ctg agc agc cag tta aaa cct aaa cct gtg ggt gaa gaa aac atc       1070
Thr Leu Ser Ser Gln Leu Lys Pro Lys Pro Val Gly Glu Glu Asn Ile
                     320                    325                    330
tgt ttg gat ttg aag agc ta aagagtctgc agcaggattg gagactgact       1120
Cys Leu Asp Leu Lys Ser
             335
```

```
tgtgactgcg ggctgggggg gcattcccag taggaatgtg aagccagagg tttcggattc    1180

gtgacatcca cccctgggc aagtgagagc atctgcaaaa tgcaaagaga actacctcat    1240

atgcaggatg agccaatggc agtctcaaga aatgtactcg ggcgacacct tacctgtgga    1300

aagcaaatct tttcaaaata agccactggg actcggtagg tggagcccca gctgctcttc    1360

tagggaccta tggggccttc gtggcatctc tgtgctgtgt gctggggagg aggttgatgt    1420

aatggtgact cttttctgat cagcaccttg gccgtgattc ccaaggtccc agccaaagca    1480

aagggccagt tgtttcagtt taaacagaca tgtctttagt ctaataaaat tagttaactg    1540

ccagtaaagt tatttgttag ctttgatgaa agctatgttg gtatctttcc ctaatcatca    1600

aagtaaataa aaaatcattt ct                                           1622
```

<210> 142

<211> 2475

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36)... (746)

<400> 142

```
acctgtggga gcgacccggg agaaggaggg ccaag atg gcg gaa gcg gag gag       53
                                         Met Ala Glu Ala Glu Glu
                                         1               5

tct cca gga gac ccg ggg aca gca tcg ccc agg ccc ctg ttt gca ggc     101
Ser Pro Gly Asp Pro Gly Thr Ala Ser Pro Arg Pro Leu Phe Ala Gly
            10              15              20

ctt tca gat ata tcc atc tca caa gac atc ccc gta gaa gga gaa atc     149
```

Leu Ser Asp Ile Ser Ile Ser Gln Asp Ile Pro Val Glu Gly Glu Ile

       25   30   35

acc att cct atg aga tct cgc atc cgg gag ttt gac agc tcc aca tta   197

Thr Ile Pro Met Arg Ser Arg Ile Arg Glu Phe Asp Ser Ser Thr Leu

       40   45   50

aat gaa tct gtt cgc aat acc atc atg cgt gat cta aaa gct gtt ggg   245

Asn Glu Ser Val Arg Asn Thr Ile Met Arg Asp Leu Lys Ala Val Gly

  55   60   65   70

aaa aaa ttc atg cat gtt ttg tac cca agg aaa agt aat act ctt ttg   293

Lys Lys Phe Met His Val Leu Tyr Pro Arg Lys Ser Asn Thr Leu Leu

                75   80   85

aga gat tgg gat ttg tgg ggc cct ttg atc ctt tgt gtg aca ctc gca   341

Arg Asp Trp Asp Leu Trp Gly Pro Leu Ile Leu Cys Val Thr Leu Ala

                90   95   100

tta atg ctg caa aga gac tct gca gat agt gaa aaa gat gga ggg ccc   389

Leu Met Leu Gln Arg Asp Ser Ala Asp Ser Glu Lys Asp Gly Gly Pro

              105   110   115

caa ttt gca gag gtg ttt gtc att gtc tgg ttt ggt gca gtt acc atc   437

Gln Phe Ala Glu Val Phe Val Ile Val Trp Phe Gly Ala Val Thr Ile

              120   125   130

acc ctc aac tca aaa ctt ctt gga ggg aac ata tct ttt ttt cag agc   485

Thr Leu Asn Ser Lys Leu Leu Gly Gly Asn Ile Ser Phe Phe Gln Ser

135   140   145   150

ctc tgt gtg ctg ggt tac tgt ata ctt ccc ttg aca gta gca atg ctg   533

Leu Cys Val Leu Gly Tyr Cys Ile Leu Pro Leu Thr Val Ala Met Leu

```
                    155                   160                   165
att tgc cgg ctg gta ctt ttg gct gat cca gga cct gta aac ttc atg     581
Ile Cys Arg Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn Phe Met
                    170                   175                   180
gtt cgg ctt ttt gtg gtg att gtg atg ttt gcc tgg tct ata gtt gcc     629
Val Arg Leu Phe Val Val Ile Val Met Phe Ala Trp Ser Ile Val Ala
                    185                   190                   195
tcc aca gct ttc ctt gct gat agc cag cct cca aac cgc aga gcc cta     677
Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg Ala Leu
                    200                   205                   210
gct gtt tat cct gtt ttc ctg ttt tac ttt gtc atc agt tgg atg att     725
Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp Met Ile
215                 220                   225                   230
ctc acc ttt act cct cag taaatca ggaatgggaa attaaaaacc agtgaattga     780
Leu Thr Phe Thr Pro Gln
                    235
aagcacatct gaaagatgca attcaccatg gagctttgtc tctggccctt atttgtctaa     840
ttttggaggt atttgataac tgagtaggtg aggagattaa aagggagcca tatagcactg     900
tcaccccctta tttgaggaac tgatgtttga aaggctgttc ttttctctct taatgtcatt     960
tctttaaaaa tacatgtgca tactacacac agtatataat gcctccttaa ggcatgatgg    1020
agtcaccgtg gtccatttgg gtgacaacca gtgacttggg aagcacatag atacatctta    1080
caagttgaat agagttgata actattttca gttttgagaa taccagttca ggtgcagctc    1140
ttaaacacat tgccttatga ctattagaat atgcctctct tttcataaat aaaaatacat    1200
ggtctatatc cattttcttt tatttctctc tcttaagctt aaaaaggcaa tgagagaggt    1260
taggagtggg ttcatacacg gagaatgaga aaacatgcat taaccaatat tcagattttg    1320
```

```
atcaggggaa attctacact tgttgcaaaa aaaaaaaaaa aaaaagcaaa gggcctctaa   1380

agaatcagcc tctttggtcc ctttgtgctg tcaccttttt gccatgttta acagcatctt   1440

ggttggcact ctagtcttaa tcttgctcct taactttgaa tatgcagtct aaaatgtcag   1500

tagtcaacat gtaattttcc tttgaaattc tgaatattcc agtgctggaa cttatccaaa   1560

aagaagacct cagaaactta gattggtaga tctctagtgc atattatcat gtgggcacct   1620

tctcttaggg tggaatgagg cagtctggat gcagcatagt taaaaggagc tgtttaatat   1680

tctctgtagt ctggcctctt aactagaaag taaagctaaa tcagaagcct gtatttaacc   1740

atgtgaacag ggagggattt agtgttctga tggctgatta atagaacagc tagatactta   1800

gagcatgacg tgggatggga tgagtttaca gctgctgcct tttcatggtg agcttagcag   1860

ttttctcatt agatgtgttt ttttgggttg gggaatagca atttattta ttgattttag   1920

actttatcaa gctaattagc tcccctttag ataagtacat gttgcacatg tgcacctact   1980

tgtaatctca gatatttatg cacacaagtg tgaaggtttt tcagggagca gagcatctgg   2040

gacaggctga ttctgagcta aacagggctc ctttaaggca atatgaactg ttgccttcta   2100

taaattgcac attgaggaac tctaatagac aaagattagg tgtcaggcag aaaacactca   2160

ttgtaaatat actattagtt gataaacata ggactttctt attccccagt ttttctttat   2220

catataattt aaatatttat tcattttgta tttaaagact acctacacat agatatatga   2280

ttccaaagtc atactttctc catccccaca ttagccaagt gaatacaggg ccaaatgggt   2340

tcttggaatg ataataacaa agcattacaa agtgggtccc cttggttcca gccttgtcca   2400

gagttttgg ttatatattt ctatttatta caatttacct tttaaattgt aaaataaacc    2460

tttgtgtgga cagag                                                    2475
```

<210> 143

<211> 1739

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (21)...(1703)

<400> 143

```
tgcgccctga cagcccaaca atg gcg gcg ccc gcg gag tcg ctg agg agg        50
                        Met Ala Ala Pro Ala Glu Ser Leu Arg Arg
                         1               5                  10

cgg aag act ggg tac tcg gat ccg gag cct gag tcg ccg ccc gcg ccg        98
Arg Lys Thr Gly Tyr Ser Asp Pro Glu Pro Glu Ser Pro Pro Ala Pro
                15                  20                  25

ggg cgt ggc ccc gca ggc tct ccg gcc cat ctc cac acg ggc acc ttc       146
Gly Arg Gly Pro Ala Gly Ser Pro Ala His Leu His Thr Gly Thr Phe
            30                  35                  40

tgg ctg acc cgg atc gtg ctc ctg aag gcc cta gcc ttc gtg tac ttc       194
Trp Leu Thr Arg Ile Val Leu Leu Lys Ala Leu Ala Phe Val Tyr Phe
            45                  50                  55

gtg gca ttc ctg gtg gct ttc cat cag aac aag cag ctc atc ggt gac       242
Val Ala Phe Leu Val Ala Phe His Gln Asn Lys Gln Leu Ile Gly Asp
        60                  65                  70

agg ggg ctg ctt ccc tgc aga gtg ttc ctg aag aac ttc cag cag tac       290
Arg Gly Leu Leu Pro Cys Arg Val Phe Leu Lys Asn Phe Gln Gln Tyr
    75                  80                  85                  90

ttc cag gac agg acg agc tgg gaa gtc ttc agc tac atg ccc acc atc       338
Phe Gln Asp Arg Thr Ser Trp Glu Val Phe Ser Tyr Met Pro Thr Ile
                95                  100                 105
```

ctc tgg ctg atg gac tgg tca gac atg aac tcc aac ctg gac ttg ctg   386
Leu Trp Leu Met Asp Trp Ser Asp Met Asn Ser Asn Leu Asp Leu Leu
            110   115   120

gct ctt ctc gga ctg ggc atc tcg tct ttc gta ctg atc acg ggc tgc   434
Ala Leu Leu Gly Leu Gly Ile Ser Ser Phe Val Leu Ile Thr Gly Cys
            125   130   135

gcc aac atg ctt ctc atg gct gcc ctg tgg ggc ctc tac atg tcc ctg   482
Ala Asn Met Leu Leu Met Ala Ala Leu Trp Gly Leu Tyr Met Ser Leu
        140   145   150

gtt aat gtg ggc cat gtc tgg tac tct ttc gga tgg gag tcc cag ctt   530
Val Asn Val Gly His Val Trp Tyr Ser Phe Gly Trp Glu Ser Gln Leu
155   160   165   170

ctg gag acg ggg ttc ctg ggg atc ttc ctg tgc cct ctg tgg acg ctg   578
Leu Glu Thr Gly Phe Leu Gly Ile Phe Leu Cys Pro Leu Trp Thr Leu
            175   180   185

tca agg ctg ccc cag cat acc ccc aca tcc cgg att gtc ctg tgg ggc   626
Ser Arg Leu Pro Gln His Thr Pro Thr Ser Arg Ile Val Leu Trp Gly
            190   195   200

ttc cgg tgg ctg atc ttc agg atc atg ctt gga gca ggc ctg atc aag   674
Phe Arg Trp Leu Ile Phe Arg Ile Met Leu Gly Ala Gly Leu Ile Lys
            205   210   215

atc cgg ggg gac cgg tgc tgg cga gac ctc acc tgc atg gac ttc cac   722
Ile Arg Gly Asp Arg Cys Trp Arg Asp Leu Thr Cys Met Asp Phe His
        220   225   230

tat gag acc cag ccg atg ccc aat cct gtg gca tac tac ctg cac cac   770

```
        Tyr Glu Thr Gln Pro Met Pro Asn Pro Val Ala Tyr Tyr Leu His His
        235             240             245             250

        tca ccc tgg tgg ttc cat cgc ttc gag acg ctc agc aac cac ttc atc      818
        Ser Pro Trp Trp Phe His Arg Phe Glu Thr Leu Ser Asn His Phe Ile
                    255             260             265

        gag ctc ctg gtg ccc ttc ttc ctc ttc ctc ggc cgg cgg gcg tgc atc      866
        Glu Leu Leu Val Pro Phe Phe Leu Phe Leu Gly Arg Arg Ala Cys Ile
                        270             275             280

        atc cac ggg gtg ctg cag atc ctg ttc cag gcc gtc ctc atc gtc agc      914
        Ile His Gly Val Leu Gln Ile Leu Phe Gln Ala Val Leu Ile Val Ser
                        285             290             295

        ggg aac ctc agc ttc ctg aac tgg ctg act atg gtg ccc agc ctg gcc      962
        Gly Asn Leu Ser Phe Leu Asn Trp Leu Thr Met Val Pro Ser Leu Ala
                    300             305             310

        tgc ttt gat gac gcc acc ctg gga ttc ttg ttc ccc tct ggg cca ggc     1010
        Cys Phe Asp Asp Ala Thr Leu Gly Phe Leu Phe Pro Ser Gly Pro Gly
        315             320             325             330

        agc ctg aag gac cga gtt ctg cag atg cag agg gac atc cga ggg gcc     1058
        Ser Leu Lys Asp Arg Val Leu Gln Met Gln Arg Asp Ile Arg Gly Ala
                        335             340             345

        cgg ccc gag ccc aga ttc ggc tcc gtg gtg cgg cgt gca gcc aac gtc     1106
        Arg Pro Glu Pro Arg Phe Gly Ser Val Val Arg Arg Ala Ala Asn Val
                        350             355             360

        tcg ctg ggc gtc ctg ctg gcc tgg ctc agc gtg ccc gtg gtc ctc aac     1154
        Ser Leu Gly Val Leu Leu Ala Trp Leu Ser Val Pro Val Val Leu Asn
```

```
              365                      370                      375
ttg ctg agc tcc agg cag gtc atg aac acc cac ttc aac tct ctt cac       1202
Leu Leu Ser Ser Arg Gln Val Met Asn Thr His Phe Asn Ser Leu His
          380                      385                      390
atc gtc aac act tac ggg gcc ttc gga agc atc acc aag gag cgg gcg       1250
Ile Val Asn Thr Tyr Gly Ala Phe Gly Ser Ile Thr Lys Glu Arg Ala
395                      400                      405                      410
gag gtg atc ctg cag ggc aca gcc agc tcc aac gcc agc gcc ccc gat       1298
Glu Val Ile Leu Gln Gly Thr Ala Ser Ser Asn Ala Ser Ala Pro Asp
                  415                      420                      425
gcc atg tgg gag gac tac gag ttc aag tgc aag cca ggt gac ccc agc       1346
Ala Met Trp Glu Asp Tyr Glu Phe Lys Cys Lys Pro Gly Asp Pro Ser
                  430                      435                      440
aga cgg ccc tgc ctc atc tcc ccg tac cac tac cgc ctg gac tgg ctg       1394
Arg Arg Pro Cys Leu Ile Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu
              445                      450                      455
atg tgg ttc gcg gcc ttc cag acc tac gag cac aac gac tgg atc atc       1442
Met Trp Phe Ala Ala Phe Gln Thr Tyr Glu His Asn Asp Trp Ile Ile
          460                      465                      470
cac ctg gct ggc aag ctc ctg gcc agc gac gcc gag gcc ttg tcc ctg       1490
His Leu Ala Gly Lys Leu Leu Ala Ser Asp Ala Glu Ala Leu Ser Leu
475                      480                      485                      490
ctg gca cac aac ccc ttc gcg ggc agg ccc ccg ccc agg tgg gtc cga       1538
Leu Ala His Asn Pro Phe Ala Gly Arg Pro Pro Pro Arg Trp Val Arg
              495                      500                      505
```

```
gga gag cac tac agg tac aag ttc agc cgt cct ggg ggc agg cac gcc        1586
Gly Glu His Tyr Arg Tyr Lys Phe Ser Arg Pro Gly Gly Arg His Ala
            510                 515                 520

gcc gag ggc aag tgg tgg gtg cgg aag agg atc gga gcc tac ttc cct        1634
Ala Glu Gly Lys Trp Trp Val Arg Lys Arg Ile Gly Ala Tyr Phe Pro
        525                 530                 535

ccg ctc agc ctg gag gag ctg agg ccc tac ttc agg gac cgt ggg tgg        1682
Pro Leu Ser Leu Glu Glu Leu Arg Pro Tyr Phe Arg Asp Arg Gly Trp
        540                 545                 550

cct ctg ccc ggg ccc ctc tagacgtgca ccagaaataa aggcgaagac             1730
Pro Leu Pro Gly Pro Leu
555                 560

ccagccccc                                                              1739
```

<210> 144

<211> 2005

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (107)... (1327)

<400> 144

```
ggagcccagc ggcgggtgtg agagtccgta aggagcagct tccaggatcc tgagatccgg        60

agcagccggg gtcggagcgg ctcctcaaga gttactgatc tatgaa atg gca gag        115
                                                         Met Ala Glu
```

1

aat gga aaa aat tgt gac cag aga cgt gta gca atg aac aag gaa cat   163
Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn Lys Glu His
        5   10   15

cat aat gga aat ttc aca gac ccc tct tca gtg aat gaa aag aag agg   211
His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg
20   25   30   35

agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag ccg ctc   259
Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu
                40   45   50

att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg aag gaa   307
Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu
                55   60   65

tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct ttt tta   355
Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser Phe Leu
                70   75   80

ctg ctg ctt gct gtg ctt ata gct acg tat tat gtt gaa gga gtg cat   403
Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu Gly Val His
        85   90   95

caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat gcc tac   451
Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr Ala Tyr
100   105   110   115

tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca ggg ctg   499
Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr Gly Leu
                120   125   130

```
cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt aca tta        547
His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val Thr Leu
                135             140             145

gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc tat cct        595
Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro Tyr Pro
            150             155             160

gat cag att att tgt cca gat gaa gag ggc act gaa gga acc att tct        643
Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr Ile Ser
            165             170             175

ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg tgg ggt        691
Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met Trp Gly
180             185             190                 195

atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc aga gca       739
Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala Arg Ala
                200             205             210

gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag gaa ttt       787
Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln Glu Phe
                215             220             225

gaa gag atg ctg gaa cat gca gag tct gca caa gac ttt gcc tcc cgg       835
Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe Ala Ser Arg
            230             235             240

gcc aaa ctg gca gtt caa aaa cta gta cag aaa gtt gga ttt ttt gga       883
Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly Phe Phe Gly
            245             250             255

att ttg gcc tgt gct tca att cca aat cct tta ttt gat ctg gct gga       931
```

292/307

Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp Leu Ala Gly

260   265   270   275

ata acg tgt gga cac ttt ctg gta cct ttt tgg acc ttc ttt ggt gca   979

Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe Phe Gly Ala

                       280   285   290

acc cta att gga aaa gca ata ata aaa atg cat atc cag aaa att ttt   1027

Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln Lys Ile Phe

                       295   300   305

gtt ata ata aca ttc agc aag cac ata gtg gag caa atg gtg gct ttc   1075

Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met Val Ala Phe

                       310   315   320

att ggt gct gtc ccc ggc ata ggt cca tct ctg cag aag cca ttt cag   1123

Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys Pro Phe Gln

                       325   330   335

gag tac ctg gag gct caa cgg cag aag ctt cac cac aaa agc gaa atg   1171

Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys Ser Glu Met

340   345   350   355

ggc aca cca cag gga gaa aac tgg ttg tcc tgg atg ttt gaa aag ttg   1219

Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu Lys Leu

                       360   365   370

gtc gtt gtc atg gtg tgt tac ttc atc cta tct atc att aac tcc atg   1267

Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn Ser Met

                       375   380   385

gca caa agt tat gcc aaa cga atc cag cag cgg ttg aac tca gag gag   1315

Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser Glu Glu

```
          390                 395                 400

aaa act aaa taagta gagaaagttt taaactgcag aaattggagt ggatgggttc        1370
Lys Thr Lys

          405

tgccttaaat tgggaggact ccaagccggg aaggaaaatt ccctttttcca acctgtatca    1430

attttttacaa ctttttttcct gaaagcagtt tagtccatac tttgcactga catacttttt   1490

ccttctgtgc taaggtaagg tatccaccct cgatgcaatc caccttgtgt tttcttaggg     1550

tggaatgtga tgttcagcag caaacttgca acagactggc cttctgtttg ttactttcaa     1610

aaggcccaca tgatacaatt agagaattcc caccgcacaa aaaaagttcc taagtatgtt     1670

aaatatgtca agcttttttag gcttgtcaca aatgattgct ttgttttcct aagtcatcaa    1730

aatgtatata aattatctag attggataac agtcttgcat gtttatcatg ttacaattta     1790

atattccatc ctgcccaacc cttcctctcc catcctcaaa aaagggccat tttatgatgc     1850

attgcacacc ctctggggaa attgatcttt aaattttgag acagtataag gaaaatctgg     1910

ttggtgtctt acaagtgagc tgacaccatt ttttattctg tgtatttaga atgaagtctt     1970

gaaaaaaact ttataaagac atctttaatc attcc                                2005
```

```
<210> 145

<211> 1558

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (31)...(1392)

<400> 145

tcccggtcgg gtgcaaggag ccgaggcgag atg ggc gtc ctg ggc cgg gtc ctg      54
```

```
                              Met Gly Val Leu Gly Arg Val Leu

                               1                    5

ctg tgg ctg cag ctc tgc gca ctg acc cag gcg gtc tcc aaa ctc tgg      102

Leu Trp Leu Gln Leu Cys Ala Leu Thr Gln Ala Val Ser Lys Leu Trp

        10                  15                  20

gtc ccc aac acg gac ttc gac gtc gca gcc aac tgg agc cag aac cgg      150

Val Pro Asn Thr Asp Phe Asp Val Ala Ala Asn Trp Ser Gln Asn Arg

 25                  30                  35                  40

acc ccg tgc gcc ggc ggc gcc gtt gag ttc ccg gcg gac aag atg gtg      198

Thr Pro Cys Ala Gly Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val

                    45                  50                  55

tca gtc ctg gtg caa gaa ggt cac gcc gtc tca gac atg ctc ctg ccg      246

Ser Val Leu Val Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro

                60                  65                  70

ctg gat ggg gaa ctc gtc ctg gct tca gga gcc gga ttc ggc gtc tca      294

Leu Asp Gly Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser

            75                  80                  85

gac gtg ggc tcg cac ctg gac tgt ggc gcg ggc gaa cct gcc gtc ttc      342

Asp Val Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe

        90                  95                  100

cgc gac tct gac cgc ttc tcc tgg cat gac ccg cac ctg tgg cgc tct      390

Arg Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser

105                  110                  115                  120

ggg gac gag gca cct ggc ctc ttc ttc gtg gac gcc gag cgc gtg ccc      438

Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val Pro
```

```
                    125                 130                 135
tgc cgc cac gac gac gtc ttc ttt ccg cct agt gcc tcc ttc cgc gtg      486
Cys Arg His Asp Asp Val Phe Phe Pro Pro Ser Ala Ser Phe Arg Val
                  140                 145                 150
ggg ctc ggc cct ggc gct agc ccc gtg cgt gtc cgc agc atc tcg gct      534
Gly Leu Gly Pro Gly Ala Ser Pro Val Arg Val Arg Ser Ile Ser Ala
                155                 160                 165
ctg ggc cgg acg ttc acg cgc gac gag gac ctg gct gtt ttc ctg gcg      582
Leu Gly Arg Thr Phe Thr Arg Asp Glu Asp Leu Ala Val Phe Leu Ala
              170                 175                 180
tcc cgc gcg ggc cgc cta cgc ttc cac ggg ccg ggc gcg ctg agc gtg      630
Ser Arg Ala Gly Arg Leu Arg Phe His Gly Pro Gly Ala Leu Ser Val
185                 190                 195                 200
ggc ccc gag gac tgc gcg gac ccg tcg ggc tgc gtc tgc ggc aac gcg      678
Gly Pro Glu Asp Cys Ala Asp Pro Ser Gly Cys Val Cys Gly Asn Ala
                  205                 210                 215
gag gcg cag ccg tgg atc tgc gcg gcc ctg ctc cag ccc ctg ggc ggc      726
Glu Ala Gln Pro Trp Ile Cys Ala Ala Leu Leu Gln Pro Leu Gly Gly
                220                 225                 230
cgc tgc ccc cag gcc gcc tgc cac agc gcc ctc cgg ccc cag ggg cag      774
Arg Cys Pro Gln Ala Ala Cys His Ser Ala Leu Arg Pro Gln Gly Gln
              235                 240                 245
tgc tgt gac ctc tgt gga gcc gtt gtg ttg ctg acc cac ggc ccc gca      822
Cys Cys Asp Leu Cys Gly Ala Val Val Leu Leu Thr His Gly Pro Ala
            250                 255                 260
```

```
ttt gac ctg gag cgg tac cgg gcg cgg ata ctg gac acc ttc ctg ggt         870
Phe Asp Leu Glu Arg Tyr Arg Ala Arg Ile Leu Asp Thr Phe Leu Gly
265             270             275             280

ctg cct cag tac cac ggg ctg cag gtg gcc gtg tcc aag gtg cca cgc         918
Leu Pro Gln Tyr His Gly Leu Gln Val Ala Val Ser Lys Val Pro Arg
            285             290             295

tcg tcc cgg ctc cgt gag gcc gat acg gag atc cag gtg gtg ctg gtg         966
Ser Ser Arg Leu Arg Glu Ala Asp Thr Glu Ile Gln Val Val Leu Val
            300             305             310

gag aat ggg ccc gag aca ggc gga gcg ggg cgg ctg gcc cgg gcc ctc        1014
Glu Asn Gly Pro Glu Thr Gly Gly Ala Gly Arg Leu Ala Arg Ala Leu
            315             320             325

ctg gcg gac gtc gcc gag aac ggc gag gcc ctc ggc gtc ctg gag gcg        1062
Leu Ala Asp Val Ala Glu Asn Gly Glu Ala Leu Gly Val Leu Glu Ala
            330             335             340

acc atg cgg gag tcg ggc gca cac gtc tgg ggc agc tcc gcg gct ggg        1110
Thr Met Arg Glu Ser Gly Ala His Val Trp Gly Ser Ser Ala Ala Gly
345             350             355             360

ctg gcg ggc ggc gtg gcg gct gcc gtg ctg ctg gcg ctg ctg gtc ctg        1158
Leu Ala Gly Gly Val Ala Ala Ala Val Leu Leu Ala Leu Leu Val Leu
            365             370             375

ctg gtg gcg ccg ccg ctg ctg cgc cgc gcg ggg agg ctc agg tgg agg        1206
Leu Val Ala Pro Pro Leu Leu Arg Arg Ala Gly Arg Leu Arg Trp Arg
            380             385             390

agg cac gag gcg gcg gcc ccg gct gga gcg ccc ctc ggc ttc cgc aac        1254
```

```
Arg His Glu Ala Ala Ala Pro Ala Gly Ala Pro Leu Gly Phe Arg Asn

         395                 400                 405

ccg gtg ttc gac gtg acg gcc tcc gag gag ctg ccc ctg ccg cgg cgg    1302

Pro Val Phe Asp Val Thr Ala Ser Glu Glu Leu Pro Leu Pro Arg Arg

         410                 415                 420

ctc agc ctg gtt ccg aag gcg gcc gca gac agc acc agc cac agt tac    1350

Leu Ser Leu Val Pro Lys Ala Ala Ala Asp Ser Thr Ser His Ser Tyr

425             430                 435                 440

ttc gtc aac cct ctg ttc gcc ggg gcc gag gcc gag gcc t gagcggccgc   1400

Phe Val Asn Pro Leu Phe Ala Gly Ala Glu Ala Glu Ala

                 445                 450

ctgaccgtcg accttggggc tctccacccc ctctggcccc agtcgaactg ggggctagcc   1460

acctcctcgt ccagccccca aacctcccct tcctttcccc ctcctccggg ggccaaggac   1520

agggtggcct tactcagtaa aggtgtttcc tgcacctg                           1558
```

<210> 146

<211> 1005

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151)...(330)

<400> 146

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attcctgtaa tggctgcttc ctagaaggtc gtgtcacgtg gaacctctta atctcagcat    60

ccggagctcc aggaagggaa aatttcaagt cagatagaat tctatatata ccatttcttt   120
```

```
ggaaccttca gccctcaaga ttccaacatc atg acc tca gtt tca aca cag ttg      174
                                    Met Thr Ser Val Ser Thr Gln Leu
                                     1                   5

tcc tta gtc ctc atg tca ctg ctt ttg gtg ctg cct gtt gtg gaa gca       222
Ser Leu Val Leu Met Ser Leu Leu Leu Val Leu Pro Val Val Glu Ala
     10                  15                  20

gta gaa gcc ggt gat gca atc gcc ctt ttg tta ggt gtg gtt ctc agc       270
Val Glu Ala Gly Asp Ala Ile Ala Leu Leu Leu Gly Val Val Leu Ser
 25                  30                  35                  40

att aca ggc att tgt gcc tgc ttg ggg gta tat gca cga aaa aga aat       318
Ile Thr Gly Ile Cys Ala Cys Leu Gly Val Tyr Ala Arg Lys Arg Asn
                 45                  50                  55

gga cag atg tga ctttgaaagg cctactgagt caaacctcac cctgaaaacc          370
Gly Gln Met

tttgcgcttt agaggctaaa cctgagattt ggtgtgtgaa aggttccaag aatcagtaaa    430

taagggagtt tcacattttt cattgtttcc atgaaatggc aacaaacata catttataaa    490

ttgaaaaaaa aatgttttct ttacaacaaa taatgcacag aaaaatgcag cctataattt    550

gctagttagg tagtcaaaga agtaagatgg ctgaaattta cataagtaat atttcataat    610

cttagaattc tctcaaagca tgtgaaatag gaagaaggaa gttcttgccc agaatcttag    670

gaaatcacca ctgttcggtt ataatcactg cctcctgaat cgttgaggag tcttttaaat    730

tagatttttg ttttgttgtc tcccaagtta atattatatt tagatatcag agagtcaggc    790

aaaaaggaaa acttttatct ctagggaaaa aacatttaga aaaatgtatt cagtgtatct    850

aatactgaaa tgcggaaaaa aatttaatgt taaaaaaaaa actatagaca ttgacatgga    910

aaagagattt aatgttttga aaaaaaactt tatattaact gagtaacatc ctcctgatga    970

gaagtactat attaaatata aacccattat gttat                             1005
```

<210> 147

<211> 969

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151)... (783)

<400> 147

```
gctggacacc tggagctgcc cgaggacgcg gaggagagac ccgagggtcg ccgctggtag      60

ggtcgctcag ccctgccgtc cttcaccacc acaccttcac ctgcgcccag ctccctgcgc     120

gcctggacag cgcctgctgc ccgcctcccg atg gcc ctg ccc cag atg tgt gac     174
                                    Met Ala Leu Pro Gln Met Cys Asp
                                     1                   5

ggg agc cac ttg gcc tcc acc ctc cgc tat tgc atg aca gtc agc ggc     222
Gly Ser His Leu Ala Ser Thr Leu Arg Tyr Cys Met Thr Val Ser Gly
        10                  15                  20

aca gtg gtt ctg gtg gcc ggg acg ctc tgc ttc gct tgg tgg agc gaa     270
Thr Val Val Leu Val Ala Gly Thr Leu Cys Phe Ala Trp Trp Ser Glu
25                  30                  35                  40

ggg gat gca acc gcc cag cct ggc cag ctg gcc cca ccc acg gag tat     318
Gly Asp Ala Thr Ala Gln Pro Gly Gln Leu Ala Pro Pro Thr Glu Tyr
                45                  50                  55

ccg gtg cct gag ggc ccc agc ccc ctg ctc agg tcc gtc agc ttc gtc     366
Pro Val Pro Glu Gly Pro Ser Pro Leu Leu Arg Ser Val Ser Phe Val
```

		60				65				70						

tgc tgc ggt gca ggt ggc ctg ctg ctg ctc att ggc ctg ctg tgg tcc   414

Cys Cys Gly Ala Gly Gly Leu Leu Leu Leu Ile Gly Leu Leu Trp Ser

			75			·		80				85			

gtc aag gcc agc atc cca ggg cca cct cga tgg gac ccc tat cac ctc   462

Val Lys Ala Ser Ile Pro Gly Pro Pro Arg Trp Asp Pro Tyr His Leu

	90				95				100						

tcc aga gac ctg tac tac ctc act gtg gag tcc tca gag aag gag agc   510

Ser Arg Asp Leu Tyr Tyr Leu Thr Val Glu Ser Ser Glu Lys Glu Ser

105				110				115				120			

tgc agg acc ccc aaa gtg gtt gac atc ccc act tac gag gaa gcc gtg   558

Cys Arg Thr Pro Lys Val Val Asp Ile Pro Thr Tyr Glu Glu Ala Val

			125				130				135				

agc ttc cca gtg gcc gag ggg ccc cca aca cca cct gca tac cct acg   606

Ser Phe Pro Val Ala Glu Gly Pro Pro Thr Pro Pro Ala Tyr Pro Thr

		140				145				150					

gag gaa gcc ctg gag cca agt gga tcg agg gat gcc ctg ctc agc acc   654

Glu Glu Ala Leu Glu Pro Ser Gly Ser Arg Asp Ala Leu Leu Ser Thr

		155				160				165					

cag ccc gcc tgg cct cca ccc agc tat gag agc atc agc ctt gct ctt   702

Gln Pro Ala Trp Pro Pro Pro Ser Tyr Glu Ser Ile Ser Leu Ala Leu

	170				175				180						

gat gcc gtt tct gca gag acg aca ccg agt gcc aca cgc tcc tgc tca   750

Asp Ala Val Ser Ala Glu Thr Thr Pro Ser Ala Thr Arg Ser Cys Ser

185				190				195				200			

```
ggc ctg gtt cag act gca cgg gga gga agt taaaggctcc tagcaggtcc        800
Gly Leu Val Gln Thr Ala Arg Gly Gly Ser
                   205                    210
```

```
tgaatccaga gacaaaaatg ctgtgccttc tccagagtct tatgcagtgc ctgggacaca    860

gtaggcactc agcaaacgtt cgttgttgaa ggctgttcta tttatctatt gctgtataac    920

aaaccacccc agaatttagt ggcttaaaat aaatcccatt ttattatgt                969
```

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<210> 148

<211> 1241

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (20)...(517)

<400> 148
```

```
atttcggggc ggtaccaag atg gac tcc tcg cgg gcc cga cag cag ctc cgg    52
                      Met Asp Ser Ser Arg Ala Arg Gln Gln Leu Arg
                       1               5                   10
```

```
cgg cga ttc ctc ctc ctg ccg gac gcc gag gcc cag ctg gac cgc gag    100
Arg Arg Phe Leu Leu Leu Pro Asp Ala Glu Ala Gln Leu Asp Arg Glu
           15                  20                  25
```

```
ggt gac gcc ggg ccg gaa acc tcc aca gct gtt gag aaa aag gag aaa    148
Gly Asp Ala Gly Pro Glu Thr Ser Thr Ala Val Glu Lys Lys Glu Lys
       30                  35                  40
```

```
cct ctt cca aga ctt aat atc cat tct gga ttc tgg att ttg gca tcc    196
```

Pro Leu Pro Arg Leu Asn Ile His Ser Gly Phe Trp Ile Leu Ala Ser

    45   50   55

att gtt gtg acc tat tat gtt gac ttc ttt aaa acc ctt aaa gaa aac   244

Ile Val Val Thr Tyr Tyr Val Asp Phe Phe Lys Thr Leu Lys Glu Asn

  60   65   70   75

ttc cac act agc agc tgg ttt ctc tgt ggc agt gcc ttg ttg ctt gtc   292

Phe His Thr Ser Ser Trp Phe Leu Cys Gly Ser Ala Leu Leu Leu Val

          80   85   90

agt tta tca att gca ttt tac tgc ata gtc tac ctg gaa tgg tat tgt   340

Ser Leu Ser Ile Ala Phe Tyr Cys Ile Val Tyr Leu Glu Trp Tyr Cys

          95   100   105

gga att gga gaa tat gat gtc aag tat cca gcc ttg ata ccc att acc   388

Gly Ile Gly Glu Tyr Asp Val Lys Tyr Pro Ala Leu Ile Pro Ile Thr

       110   115   120

act gcc tcc ttt att gca gca gga att tgc ttc aac att gct tta tgg   436

Thr Ala Ser Phe Ile Ala Ala Gly Ile Cys Phe Asn Ile Ala Leu Trp

       125   130   135

cat gtg tgg tcg ttt ttc act cca ttg ttg ttg ttt acc cag ttt atg   484

His Val Trp Ser Phe Phe Thr Pro Leu Leu Leu Phe Thr Gln Phe Met

140   145   150   155

ggg gtt gtc atg ttt atc aca ctc ctt gga tgattt ccgaagagac   530

Gly Val Val Met Phe Ile Thr Leu Leu Gly

       160   165

agggtcttct atgttgccca ggctgtcttt gaactcctgg gatcaagtga tcctcctgcc   590

tcagccttcg aagtagttgg gactacaggc ccacgccacc gtgcctggct ggacatgtaa   650

```
atttgaagtg aatggttaaa catccagcta gctgaaagca tggcagaccc taacagaaaa    710

gctacagtgt gttttttgcag ctatgaagtg aatggtttcc tggggaaaat tgtgactttg    770

tataactgtt gttgaaacca gaataaatta tatttcactt gcatatgcat aaattattaa    830

aattttcaga agtcagtgat acagaagtac tattttgcaa tgttaatctg tttgagtctt    890

tggagaaagt ggtttcattg taggtacata gtgcactgtt aatattttaa acaagtagtt    950

cactcttcca tttaagggat agcagttcct tgtataaaat gactggatgt gtataaagga    1010

attatgttgt catgtgcctt taaccagctt tagtaattac tataatctca tatttatgat    1070

agtttttgtta ggtgacagga ccaaatgaaa atattttatg ttttctcatc actttagatt    1130

ttatcattat gtacattact gggttttttag catttcctaa tgtgaagttt taatcacttt    1190

taagtataca ttttttttctg tatcatttaa ataaaatatt tttataactt t    1241
```

<210> 149

<211> 1174

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (187)...(675)

<400> 149

```
ggaagccggg acgatgtccg catgacaacc gacgttggag tttggaggtg cttgccttag    60

agcaagggaa acagctctca ttcaaaggaa ctagaagcct ctccctcagt ggtagggaga    120

cagccaggag cggttttctg ggaactgtgg gatgtgccct tggggggcccg agaaaacaga    180
```

```
aggaag atg ctc cag acc agt aac tac agc ctg gtg ctc tct ctg cag    228
       Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln
       1               5                   10
```

ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc tca gaa ctg   276
Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu
15   20   25   30

ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc atc cag gat   324
Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp
                    35   40   45

att gca gtc ctc ttc aac atc atc atc att ttc ctc atg ttc ttc aac   372
Ile Ala Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn
                    50   55   60

acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc cat aag ttc   420
Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe
                    65   70   75

aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc agc atc tcc   468
Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser
80   85   90

ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc aac agc ttc   516
Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe
95   100   105   110

ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag aga cta gca   564
Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala
                    115   120   125

gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta aga cta ggc   612
Ala Val Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly
                    130   135   140

gat cct cac ttc tac cag gac tct ttg tgg ctg cgc aag gag ttc atg   660

Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met

        145   150   155

caa gtt cga agg tgacctct tgtcacactg atggatactt ttccttcctg   710

Gln Val Arg Arg

    160

atagaagcca catttgctgc tttgcaggga gagttggccc tatgcatggg caaacagctg   770

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cggcctccca gcgctcccaa gccgcagcgg ccgcgcccct tcagctagct cgctcgctcg   180

ctctgcttcc ctgctgccgg ctgcgcc atg gcg ttg gcg ttg gcg gcg ctg   231

                                    Met Ala Leu Ala Leu Ala Ala Leu

                                    1   5

gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag aat   279

Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln Asn

        10   15   20

gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct cca   327

Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro Pro

25   30   35   40

cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac aag   375

Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr Lys

              45   50   55

gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca aca   423

Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr Thr

              60   65   70

ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act atc   471

Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr Ile

              75   80   85

cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat ttt   519

Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp Phe

              90   95   100

gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg tta   567

Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met Leu

105   110   115   120

act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg tct   615

Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu Ser

　　　　　　　　　　　125　　　　　　　　　　130　　　　　　　　　　135

ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca gga　　663

Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser Gly

　　　　　　　　140　　　　　　　　　145　　　　　　　　　150

ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc acc　　711

Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Thr

　　　　　　155　　　　　　　　　160　　　　　　　　　165

tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg ttc　　759

Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val Phe

　　　　　170　　　　　　　　　175　　　　　　　　　180

ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat gca　　807

Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr Ala

185　　　　　　　　　190　　　　　　　　　195　　　　　　　　　200

aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc aga　　855

Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr Arg

　　　　　　　　205　　　　　　　　　210　　　　　　　　　215

gtt ctc ttt att tat taaagatgtt ttctggcaaa ggccttcctg catttatgaa　　910

Val Leu Phe Ile Tyr

　　　　　　220

ttctctctca agaagcaaga gaacacctgc aggaagtgaa tcaagatgca gaacacagag　　970

gaataatcac ctgctttaaa aaaataaagt actgttgaaa ag　　　　　　　　　　1012